```
                                                    M  K  L  Q  C  V  S  L  W     9
GAATTCCGACAAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC ATG AAG TTA CAG TGT GTT TCC CTT TGG    69

 L  L  G  T  I  L  I  L  C  S  V  D  N  H  G  L  R  R  C  L    29
CTC CTG GGT ACA ATA CTG ATA TTG TGC TCA GTA GAC AAC CAC GGT CTC AGG AGA TGT CTG   129

 I  S  T  D  M  H  H  I  E  E  S  F  Q  E  I  K  R  A  I  Q    49
ATT TCC ACA GAC ATG CAC CAT ATA GAA GAG AGT TTC CAA GAA ATC AAA AGA GCC ATC CAA   189

 A  K  D  T  F  P  N  V  T  I  L  S  T  L  E  T  L  Q  I  I    69
GCT AAG GAC ACC TTC CCA AAT GTC ACT ATC CTG TCC ACA TTG GAG ACT CTG CAG ATC ATT   249

 K  P  L  D  V  C  C  V  T  K  N  L  L  A  F  Y  V  D  R  V    89
AAG CCC TTA GAT GTG TGC TGC GTG ACC AAG AAC CTC CTG GCG TTC TAC GTG GAC AGG GTG   309

 F  K  D  H  Q  E  P  N  P  K  I  L  R  K  I  S  S  I  A  N   109
TTC AAG GAT CAT CAG GAG CCA AAC CCC AAA ATC TTG AGA AAA ATC AGC AGC ATT GCC AAC   369

 S  F  L  Y  M  Q  K  T  L  R  Q  C  Q  E  Q  R  Q  C  H  C   129
TCT TTC CTC TAC ATG CAG AAA ACT CTG CGG CAA TGT CAG GAA CAG AGG CAG TGT CAC TGC   429

 R  Q  E  A  T  N  A  T  R  V  I  H  D  N  Y  D  Q  L  E  V   149
AGG CAG GAA GCC ACC AAT GCC ACC AGA GTC ATC CAT GAC AAC TAT GAT CAG CTG GAG GTC   489

 H  A  A  A  I  K  S  L  G  E  L  D  V  F  L  A  W  I  N  K   169
CAC GCT GCT GCC ATT AAA TCC CTG GGA GAG CTC GAC GTC TTT CTA GCC TGG ATT AAT AAG   549

 N  H  E  V  M  S  S  A  *                                    178
AAT CAT GAA GTA ATG TCC TCA GCT TGA                           576

TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTTTACTGTGGGAGACAGCCCACCTTGAAGGG  655

GAAGGAGATGGGGAAGGCCCCTTGCAGCTGAAAGTCCCACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGC  734

CAAAAAGTCTACTGTGGTATTTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGC  813

CTTCCCATCTAATTTATTGTGAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCTGTAGTACACATTGT  892

ACTGAGTGGTTTTTCTGAATAAATTCCATATTTTACCTATGAAAAAAAAAAAAAAAAAAAAAAACCAGCTGAGCGCCGG  971

TCGCTACCAAAGCCGAATTC                                                              991
```

Fig. 1

```
                1                                                   50
il10-human      ~MHSSALLCC LVLLTGVRAS PGQGTQSENS CTHFPGNLPN MLRDLRDAFS
il10-mouse      ~MPGSALLCC LLLLTGMRIS RGQYSREDNN CTHFPVGQSH MLLELRTAFS
il10-viral      ~MFRASLLCC LVLLAGVWAD NKYDSESGDD CPTLPTSLPH MLHELRAAFS
mda7-mouse      MSWGLQILPC LSLILLLWNQ VPGLEGQEFR FGSCQV.TGV VLPELWEAFW
mda7-human      ~~MQMVVLPC LGFTLLLWSQ VSGAQGQEFH FGPCQV.KGV VPQKLWEAFW
     italy      ~~~~~MKLQC VSLWLL..GT ILILCSVDNH GLRRCL.IST DMHHIEESFQ
 Consensus      -M-GSALLCC L-LLL--WA- VG-LSG-ENH C-H-PV-L-- MLHELREAFS

                51                                                  100
il10-human      RVKTFFQMKD QLDN..LLLK ESLLEDFKGY LGCQALSEMI QFYLEEVMPQ
il10-mouse      QVKTFFQTKD QLDN..ILLT DSLMQDFKGY LGCQALSEMI QFYLVEVMPQ
il10-viral      RVKTFFQMKD QLDN..MLLD GSLLEDFKGY LGCQALSEMI QFYLEEVMPQ
mda7-mouse      TVKNTVQTQD DITSIRLLKP .QVLRNVSGA ESCYLAHSLL KFYLNTVFKN
mda7-human      AVKDTMQAQD NITSARLLQQ .EVLQNVSDA ESCYLVHTLL EFYLKTVFKN
     italy      EIKRAIQAKD TFPNVTILST LETLQIIKPL DVCCVTKNLL AFYVDRVFKD
 Consensus      RVKTFFQ-KD QLDN-RLLLT -SLLQDFKGY LGCQALSE-- QFYLEEV--Q

                101                                                 150
il10-human      AENQDPD..I KAHVNSLGEN LKTLRLRLRR CHRFLPCENK SKAVEQ...V
il10-mouse      AEKHGPE..I KEHLNSLGEK LKTLRMRLRR CHRFLKCENK SKAVEQ...V
il10-viral      AENHSTD.QE KDKVNSLGEK LKTLRVRLRR CHRFLPCENK SKAVEQ...V
mda7-mouse      YHSKIAKFKV LRSFSTLANN FIVIMSQLQP SKDNSMLPIS ESAHQRFLLF
mda7-human      YHNRTVEVRT LKSFSTLANN FVLIVSQLQP SQENEMFSIR DSAHRRFLLF
     italy      HQE..PNPKI LRKISSIANS FLYMQKTLRQ CQEQRQCHCR QEATNATRVI
 Consensus      AENH-P--KI -R---SL--N -KTLRSRLRR CHRFL-CENK SKAVEQFLLV

                151                                     187
il10-human      KNAFNKLQ.E KGIYKAMSEF DIFINYIEAY MTMKIRN
il10-mouse      KSDFNKLE.D QGVYKAMNEF DIFINCIEAY MMIKMKS
il10-viral      KSAFSKLQ.E KGVYKAMSEF DIFINYIEAY MTTKMKN
mda7-mouse      RRTFKQLDTE VALVKAFGEV DILLTWMQKF YHL~~~~
mda7-human      RRAFKQLDVE AALTKALGEV DILLTWMQKF YKL~~~~
     italy      HDNYDQLEVH AAAIKSLGEL DVFLAWINKN HEVMSSA
 Consensus      K-AF--L-VE ---YKAMGEF DIF-NWIE-Y MTLKMKN
```

Fig. 2

```
cgtccgccac gcgtccggac tagttctaga tcgcgagcgg ccgccctttt ttttttttt 60
ttggaagtcc taggactgat ctccaggacc agcactcttc tcccagccct tagggtcctg 120
ctcggccaag gccttccctg cc atg cga cct gtc agt gtc tgg cag tgg agc 172
ccc tgg ggg ctg ctg ctg tgc ctg ctg tgc agt tcg tgc ttg ggg tct 220
ccg tcc cct tcc acg ggc cct gag aag aag gcc ggg agc cag ggg ctt 268
cgg ttc cgg ctg gct ggc ttc ccc agg aag ccc tac gag ggc cgc gtg 316
gag ata cag cga gct ggt gaa tgg ggc acc atc tgc gat gat gac ttc 364
acg ctg cag gct gcc cac atc ctc tgc cgg gag ctg ggc ttc aca gag 412
gcc aca ggc tgg acc cac agt gcc aaa tat ggc cct gga aca ggc cgc 460
atc tgg ctg gac aac ttg agc tgc agt ggg acc gag cag agt gtg act 508
gaa tgt gcc tcc cgg ggc tgg ggg aac agt gac tgt acg cac gat gag 556
gat gct ggg gtc atc tgc aaa gac cag cgc ctc cct ggc ttc tcg gac 604
tcc aat gtc att gag gta gag cat cac ctg caa gtg gag gag gtg cga 652
att cga ccc gcc gtt ggg tgg ggc aga cga ccc ctg ccc gtg acg gag 700
ggg ctg gtg gaa gtc agg ctt cct gac ggc tgg tcg caa gtg tgc gac 748
aaa ggc tgg agc gcc cac aac agc cac gtg gtc tgc ggg atg ctg ggc 796
ttc ccc agc gaa aag agg gtc aac gcg gcc ttc tac agg ctg cta gcc 844
caa cgg cag caa cac tcc ttt ggt ctg cat ggg gtg gcg tgc gtg ggc 892
acg gag gcc cac ctc tcc ctc tgt tcc ctg gag ttc tat cgt gcc aat 940
gac acc gcc agg tgc cct ggg ggg ggc cct gca gtg gtg agc tgt gtg 988
cca ggc cct gtc tac gcg gca tcc agt ggc cag aag aag caa caa cag 1036
tcg aag cct cag ggg gag gcc cgt gtc cgt cta aag ggc ggc gcc cac 1084
cct gga gag ggc cgg gta gaa gtc ctg aag gcc agc aca tgg ggc aca 1132
gtc tgt gac cgc aag tgg gac ctg cat gca gcc agc gtg gtg tgt cgg 1180
gag ctg ggc ttc ggg agt gct cga gaa gct ctg agt ggc gct cgc atg 1228
ggg cag ggc atg ggt gct atc cac ctg agt gaa gtt cgc tgc tct gga 1276
```

Fig. 3A

cag gag ctc tcc ctc tgg aag tgc ccc cac aag aac atc aca gct gag 1324

gat tgt tca cat agc cag gat gcc ggg gtc cgg tgc aac cta cct tac 1372

act ggg gca gag acc agg atc cga ctc agt ggg ggc cgc agc caa cat 1420

gag ggg cga gtc gag gtg caa ata ggg gga cct ggg ccc ctt cgc tgg 1468

ggc ctc atc tgt ggg gat gac tgg ggg acc ctg gag gcc atg gtg gcc 1516

tgt agg caa ctg ggt ctg ggc tac gcc aac cac ggc ctg cag gag acc 1564

tgg tac tgg gac tct ggg aat ata aca gag gtg gtg atg agt gga gtg 1612

cgc tgc aca ggg act gag ctg tcc ctg gat cag tgt gcc cat cat ggc 1660

acc cac atc acc tgc aag agg aca ggg acc cgc ttc act gct gga gtc 1708

atc tgt tct gag act gca tca gat ctg ttg ctg cac tca gca ctg gtg 1756

cag gag acc gcc tac atc gaa gac cgg ccc ctg cat atg ttg tac tgt 1804

gct gcg gaa gag aac tgc ctg gcc agc tca gcc cgc tca gcc aac tgg 1852

ccc tat ggt cac cgg cgt ctg ctc cga ttc tcc tcc cag atc cac aac 1900

ctg gga cga gct gac ttc agg ccc aag gct ggg cgc cac tcc tgg gtg 1948

tgg cac gag tgc cat ggg cat tac cac agc atg gac atc ttc act cac 1996

tat gat atc ctc acc cca aat ggc acc aag gtg gct gag ggc cac aaa 2044

gct agt ttc tgt ctc gaa gac act gag tgt cag gag gat gtc tcc aag 2092

cgg tat gag tgt gcc aac ttt gga gag caa ggc atc act gtg ggt tgc 2140

tgg gat ctc tac cgg cat gac att gac tgt cag tgg att gac atc acg 2188

gat gtg aag cca gga aac tac att ctc cag gtt gtc atc aac cca aac 2236

ttt gaa gta gca gag agt gac ttt acc aac aat gca atg aaa tgt aac 2284

tgc aaa tat gat gga cat aga atc tgg gtg cac aac tgc cac att ggt 2332

gat gcc ttc agt gaa gag gcc aac agg agg ttt gaa cgc tac cct ggc 2380

cag acc agc aac cag att atc taagtgccac tgccctctgc aaaccaccac 2431

tggcccctaa tggcaggggt ctgaggctgc cattacctca ggagcttacc aagaaaccca 2491

tgtcagcaac cgcactcatc agaccatgca ctatggatgt ggaactgtca agcagaagtt 2551

Fig. 3B

```
ttcaccctcc ttcagaggcc agctgtcagt atctgtagcc aagcatggga atctttgctc 2611
ccaggcccag caccgagcag aacagaccag agcccaccac accacaaaga gcagcacctg 2671
actaactgcc cacaaaagat ggcagcagct cattttcttt aataggaggt caggatggtc 2731
agctccagta tctcccctaa gtttaggggg atacagcttt acctctagcc ttttggtggg 2791
ggaaaagatc cagccctccc acctcatttt ttactataat atgttgctag gtataatttt 2851
attttatata aaaagtgttt ctgtgattct tcagaaaaaa aaaaaaaaaa aaaaaaaaaa 2911
aaaaaaaaa                                                        2920
```

Fig. 3C

FP6-2004-686754-PUBLIC

```
Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu Leu
 1               5                  10                  15

Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly
            20                  25                  30

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly
        35                  40                  45

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly
    50                  55                  60

Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His
65                  70                  75                  80

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His
                85                  90                  95

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu
            100                 105                 110

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly
        115                 120                 125

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys
    130                 135                 140

Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val
145                 150                 155                 160

Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly
                165                 170                 175

Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg
            180                 185                 190

Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His
        195                 200                 205

Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg
    210                 215                 220

Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser
225                 230                 235                 240

Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser
                245                 250                 255

Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro
            260                 265                 270
```

Fig. 4A

```
Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala
        275                 280                 285

Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu
    290                 295                 300

Ala Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val
305                 310                 315                 320

Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Asp Arg Lys Trp
                325                 330                 335

Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser
            340                 345                 350

Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala
        355                 360                 365

Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp
    370                 375                 380

Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln
385                 390                 395                 400

Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg
                405                 410                 415

Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val
            420                 425                 430

Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp
        435                 440                 445

Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu
    450                 455                 460

Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly
465                 470                 475                 480

Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu
                485                 490                 495

Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys
            500                 505                 510

Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr Ala
        515                 520                 525

Ser Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile
    530                 535                 540
```

Fig. 4B

```
Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys
545                 550                 555                 560

Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg
                565                 570                 575

Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe
            580                 585                 590

Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly
        595                 600                 605

His Tyr His Ser Met Asp Ile Phe Thr His Tyr Asp Ile Leu Thr Pro
    610                 615                 620

Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu
625                 630                 635                 640

Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn
                645                 650                 655

Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His
            660                 665                 670

Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn
        675                 680                 685

Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser
    690                 695                 700

Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His
705                 710                 715                 720

Arg Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu Glu
                725                 730                 735

Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln Thr Ser Asn Gln Ile
            740                 745                 750

Ile
753
```

Fig. 4C

atgcgacctg tcagtgtctg gcagtggagc ccctgggggc tgctgctgtg cctgctgtgc 60

agttcgtgct tggggtctcc gtcccttcc acgggccctg agaagaaggc cgggagccag 120

gggcttcggt tccggctggc tggcttcccc aggaagccct acgagggccg cgtggagata 180

cagcgagctg gtgaatgggg caccatctgc gatgatgact tcacgctgca ggctgcccac 240

atcctctgcc gggagctggg cttcacagag gccacaggct ggacccacag tgccaaatat 300

ggccctggaa caggccgcat ctggctggac aacttgagct gcagtgggac cgagcagagt 360

gtgactgaat gtgcctcccg gggctggggg aacagtgact gtacgcacga tgaggatgct 420

ggggtcatct gcaaagacca gcgcctccct ggcttctcgg actccaatgt cattgaggta 480

gagcatcacc tgcaagtgga ggaggtgcga attcgacccg ccgttgggtg gggcagacga 540

cccctgcccg tgacggaggg gctggtggaa gtcaggcttc ctgacggctg gtcgcaagtg 600

tgcgacaaag gctggagcgc ccacaacagc cacgtggtct gcgggatgct gggcttcccc 660

agcgaaaaga gggtcaacgc ggccttctac aggctgctag cccaacggca gcaacactcc 720

tttggtctgc atggggtggc gtgcgtgggc acggaggccc acctctccct ctgttccctg 780

gagttctatc gtgccaatga caccgccagg tgccctgggg ggggccctgc agtggtgagc 840

tgtgtgccag gccctgtcta cgcggcatcc agtggccaga agaagcaaca acagtcgaag 900

cctcaggggg aggcccgtgt ccgtctaaag ggcggcgccc accctggaga gggccgggta 960

gaagtcctga aggccagcac atggggcaca gtctgtgacc gcaagtggga cctgcatgca 1020

gccagcgtgg tgtgtcggga gctgggcttc gggagtgctc gagaagctct gagtggcgct 1080

cgcatggggc agggcatggg tgctatccac ctgagtgaag ttcgctgctc tggacaggag 1140

ctctccctct ggaagtgccc ccacaagaac atcacagctg aggattgttc acatagccag 1200

gatgccgggg tccggtgcaa cctaccttac actggggcag agaccaggat ccgactcagt 1260

gggggccgca gccaacatga ggggcgagtc gaggtgcaaa taggggggacc tgggcccctt 1320

cgctggggcc tcatctgtgg ggatgactgg gggaccctgg aggccatggt ggcctgtagg 1380

caactgggtc tgggctacgc caaccacggc ctgcaggaga cctggtactg ggactctggg 1440

aatataacag aggtggtgat gagtggagtg cgctgcacag ggactgagct gtccctggat 1500

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Fig. 5A

```
cagtgtgccc atcatggcac ccacatcacc tgcaagagga cagggacccg cttcactgct 1560

ggagtcatct gttctgagac tgcatcagat ctgttgctgc actcagcact ggtgcaggag 1620

accgcctaca tcgaagaccg gcccctgcat atgttgtact gtgctgcgga agagaactgc 1680

ctggccagct cagcccgctc agccaactgg ccctatggtc accggcgtct gctccgattc 1740

tcctcccaga tccacaacct gggacgagct gacttcaggc ccaaggctgg gcgccactcc 1800

tgggtgtggc acgagtgcca tgggcattac cacagcatgg acatcttcac tcactatgat 1860

atcctcaccc caaatggcac caaggtggct gagggccaca aagctagttt ctgtctcgaa 1920

gacactgagt gtcaggagga tgtctccaag cggtatgagt gtgccaactt tggagagcaa 1980

ggcatcactg tgggttgctg ggatctctac cggcatgaca ttgactgtca gtggattgac 2040

atcacggatg tgaagccagg aaactacatt ctccaggttg tcatcaaccc aaactttgaa 2100

gtagcagaga gtgactttac caacaatgca atgaaatgta actgcaaata tgatggacat 2160

agaatctggg tgcacaactg ccacattggt gatgccttca gtgaagaggc caacaggagg 2220

tttgaacgct accctggcca gaccagcaac cagattatc                        2259
```

Fig. 5B

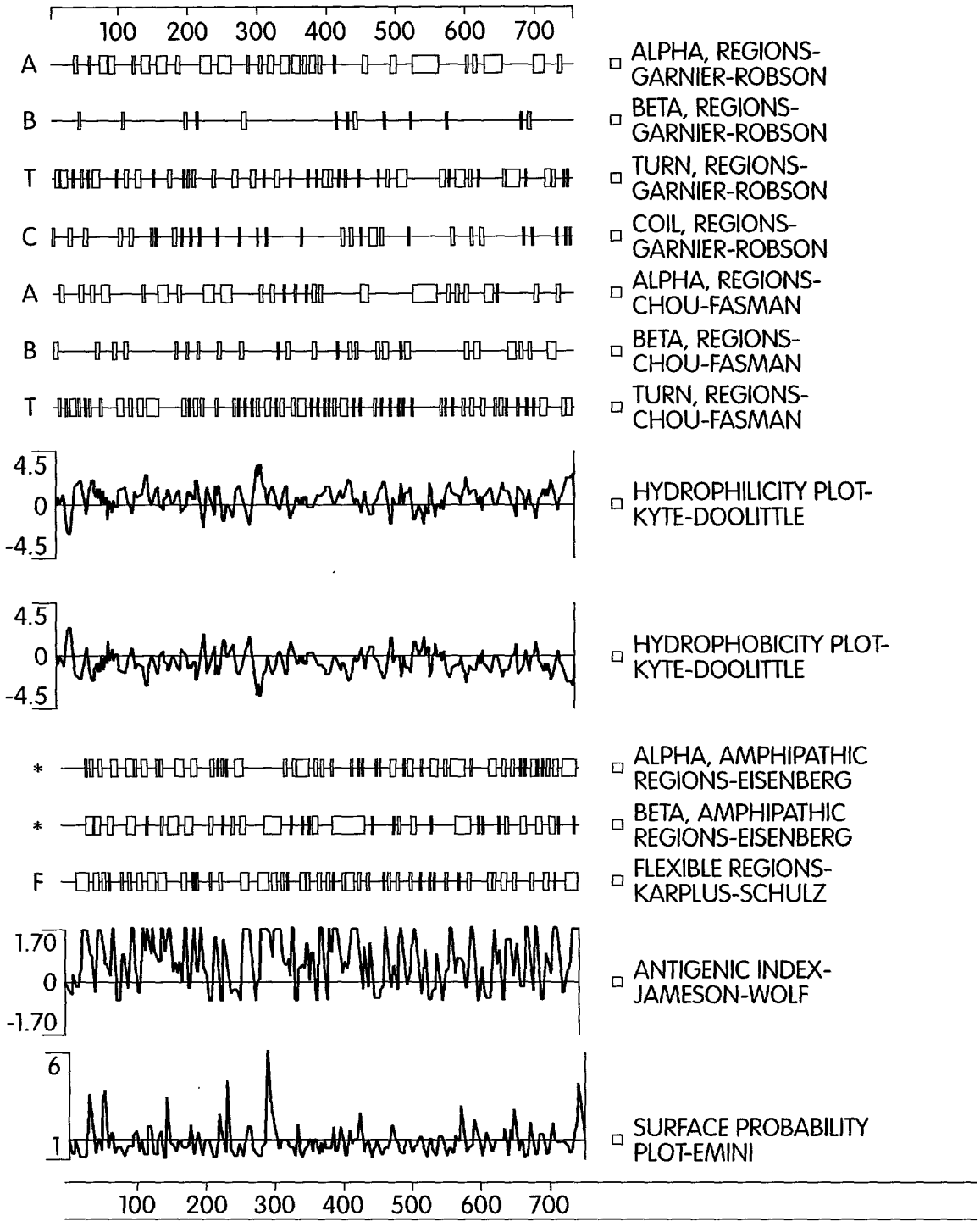

100 200 300 400 500 600 700
A
ALPHA, REGIONS-GARNIER-ROBSON
B
BETA, REGIONS-GARNIER-ROBSON
T
TURN, REGIONS-GARNIER-ROBSON
C
COIL, REGIONS-GARNIER-ROBSON
A
ALPHA, REGIONS-CHOU-FASMAN
B
BETA, REGIONS-CHOU-FASMAN
T
TURN, REGIONS-CHOU-FASMAN
4.5
0
-4.5
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
4.5
0
-4.5
HYDROPHOBICITY PLOT-KYTE-DOOLITTLE
*
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
*
BETA, AMPHIPATHIC REGIONS-EISENBERG
F
FLEXIBLE REGIONS-KARPLUS-SCHULZ
1.70
0
-1.70
ANTIGENIC INDEX-JAMESON-WOLF
6
1
SURFACE PROBABILITY PLOT-EMINI
100 200 300 400 500 600 700

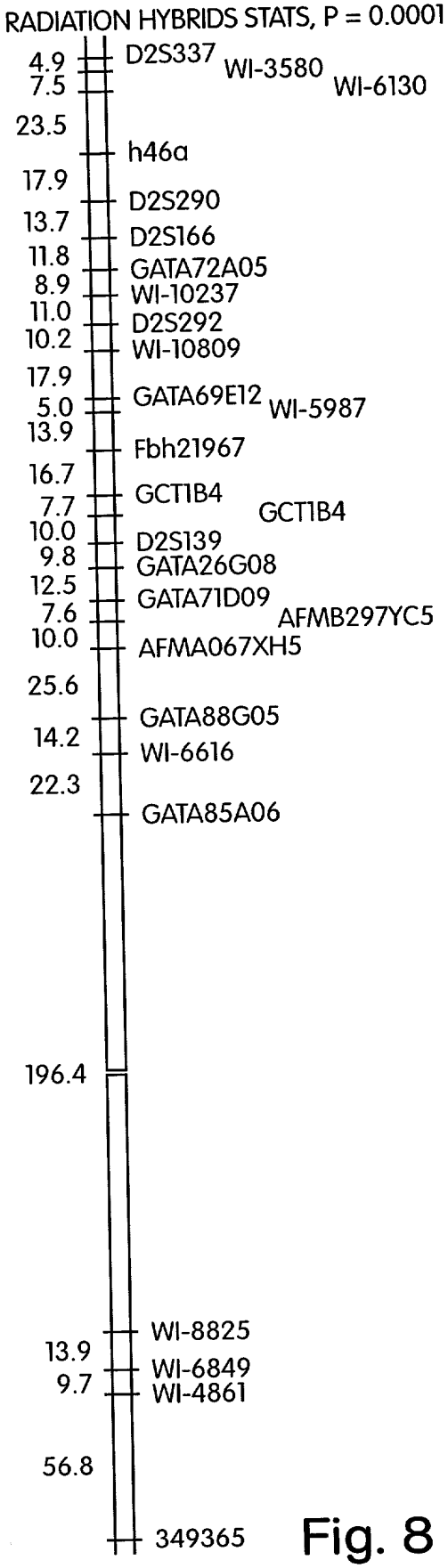
Fig. 6

```
                1                                                          60
LOX             MRFA--------WTVLLLGPLQ-----------LCALVHCAPPAAGQQQP----------
huLOL           MALA--------RGSRQLGALV-------WGACLCVHVH------GQQAQ----------
huLor           MERPLCSHLCSCLAMLALLSPLSLAQYDSWPHYPEYFQQPAPEYHQPQAPANVAKIQLRL
muLor-2         M-RAVSVWYCCPWGLLLLHCL-C----------SFSVGSPSPS-ISPEKKVGSQGLRFRL
huLor-2         M-RPVSVWQWSPWGLLL--CLLC----------SSCLGSPSPS-TGPEKKAGSQGLRFRL

               61                                                         120
LOX             ---PREPPAAPGAWRQQIQWENN-GQVFSL-----LSLGSQY-----------------
huLOL           ---P-GQGSDPARWRQLIQWENN-GQVYSL-----LNSGSEYVPA-----GPQRSESSSR
huLor           AGQKRKHSEGRVEVYYDGQWGTVCDDDFSIHAAHVVCRELGYVEAKSWTASSSYGKGEGP
muLor-2         AGFPRKPYEGRVEIQRAGEWGTICDDDFTLQAAHVLCRELGFTEATGWTHSAKYGPGTGR
huLor-2         AGFPRKPYEGRVEIQRAGEWGTICDDDFTLQAAHILCRELGFTEATGWTHSAKYGPGTGR

               121                                                        180
LOX             ------------------------QPQRRRDPGAA-------VPG---AANASAQQPRTP
huLOL           VLLA--------GAPQAQQRRSHGSPRRRQAPSLP-------LPG-RVGSDTVRGQARHP
huLor           IWLDNLHCTGNEATLAACTSNGWGVTDCKHTEDVGVVCSDKRIPGFKFDNSLINQIENLN
muLor-2         IWLDNLSCRGTEGSVTECASRGWGNSDCTHDEDAGVICKDQRLPGF--SDSNVIEVEH-Q
huLor-2         IWLDNLSCSGTEQSVTECASRGWGNSDCTHDEDAGVICKDQRLPGF--SDSNVIEVEH-H

               181                                                        240
LOX             ILL--IRD----N---------------RTAAG------RTRTAGSSGVTAG--------
huLOL           FGFGQVPD----NWREVAVGDSTGMALARTSVS------QQRHGGSASSVSAS-AFAST-
huLor           IQVEDIRIRAILSTYRKRTPVMEGYVEVKEGKTWKQICDKHWTAKNSRVVCGMFGFPGER
muLor-2         LQVEEVRLRPAVEWGRRPLPVTEGLVEVRLPEGWSQVCDKGWSAHNSHVVCGMLGFPGEK
huLor-2         LQVEEVRIRPAVGWGRRPLPVTEGLVEVRLPDGWSQVCDKGWSAHNSHVVCGMLGFPSEK

               241                                                        300
LOX             -------RP-RPTARHWF--------------------QAGY-----------STSRA
huLOL           ------YRQ-QPSYPQQFPY-----------------PQAPF----VSQYENYDPASRT
huLor           TYNTKVYKNFASRRKQRYWPFSMDCTGTEAHISSCKLGPQVSLDPMKNVTCENGLPAVVS
muLor-2         RVNMAFYRMLAQKKQHSFGLHSVACVGTEAHLSLCSLE---FYRANDTTRCSGGNPAVVS
huLor-2         RVNAAFYRLLAQRQQHSFGLHGVACVGTEAHLSLCSLE---FYRANDTARCPGGGPAVVS

               301                                                        360
LOX             ------------------REAGPSR----AENQTAPGEVPAL-----------SNLRP
huLOL           YDQGFVY----------YRPAGGGV----GAGAAAVASAGVI-----------YPYQP
huLor           CVPGQVFSPDGPSRFRKAYKPE-QPLVRLRGGAYIGEGRVEVLKNGEWGTVCDDKWDLVS
muLor-2         CVLGPLYATFTGQKKQQHSKPQGEARVRLKGGAHQGEGRVEVLKAGTWGTVCDRKWDLQA
huLor-2         CVPGPVYAASSGQKKQQQSKPQGEARVRLKGGAHPGEGRVEVLKASTWGTVCDRKWDLHA

               361                                                        420
LOX             PS----------------RVDGMVGDD-------------------PYNP-------
huLOL           RA----------------RYEEYGGGEELPEYPPQG----FYPAPERPYVPPPPPPPD
huLor           ASVVCRELGFGSAKEAVTGSRLGQGIGPIHLNEIQCTGNEKSIIDCKFNA-ESQGCNHEE
muLor-2         ASVVCPELGFGTAREALSGARMGQGMGAIHLSEVRCSGQEPSLWRCPSKNITAEDCSHSQ
huLor-2         ASVVCRELGFGSAREALSGARMGQGMGAIHLSEVRCSGQELSLWKCPHKNITAEDCSHSQ
```

Fig. 7A

```
                421                                                                480
LOX             -----YK---YSDDNPYYNYYDTYERPRPG----------GRYRP---------GYGTG
huLOL           GLDRRYSHSLYSEGTPGFE--QAYPDPGPEAAQAHGGDPRLGWYPPYANP--PPEAYGPP
huLor           DAGVRCNTP-AMGLQKKLRLNGGRNPYEGRVEVLVERNGSLVWGMVCGQNWGIVEAMVVC
muLor-2         DAGVRCNLP-YTGVETKIRLSGGRSRYEGRVEVQIGIPGHLRWGLICGDDWGTLEAMVAC
huLor-2         DAGVRCNLP-YTGAETRIRLSGGRSQHEGRVEVQIGGPGPLRWGLICGDDWGTLEAMVAC

                481                                                                540
LOX             ------Y-----------------FQ--------------------------------Y
huLOL           RALEPPY-----------------LPVRSSDTPPPGGE-------RNGAQQGRLSVGSVY
huLor           RQLGLGFASNAFQETWYWHGDVNSNKVVMSGVKCSGTELSLAHCRHDGEDVACPQGGVQY
muLor-2         RQLGLGYANHGLQETWYWDSG-NVTEVVMSGVRCTGSELSLNQCAHHSSHITCKKTGTRF
huLor-2         RQLGLGYANHGLQETWYWDSG-NITEVVMSGVRCTGTELSLDQCAHHGTHITCKRTGTRF

                541                                                                600
LOX             --------GLPDLVADPYYIQASTYVQKMSMYNLRCAAEENCLASTAYRADVRDYDHRVL
huLOL           RPNQN-GRGLPDLVPDPNYVQASTYVQRAHLYSLRCAAEEKCLASTAYAPEATDYDVRVL
huLor           GAGVACSETAPDLVLNAEMVQQTTYLEDRPMFMLQCAMEENCLSASAAQTD-PTTGYRRL
muLor-2         TAGVICSETASDLLLHSALVQETAYIEDRPLHMLYCAAEENCLASSARSAN-WPYGHRRL
huLor-2         TAGVICSETASDLLLHSALVQETAYIEDRPLHMLYCAAEENCLASSARSAN-WPYGHRRL

                601                                                                660
LOX             LRFPQRVKNQGTSDFLPSRPRYSWEWHSCHQHYHSMDEFSHYDLLDANTQRRVAEGHKAS
huLOL           LRFPQRVKNQGTADFLPNRPRHTWEWHSCHQHYHSMDEFSHYDLLDAATGKKVAEGHKAS
huLor           LRFSSQIHNNGQSDFRPKNGRHAWIWHDCHRHYHSMEVFTHYDLLNLN-GTKVAEGHKAS
muLor-2         LRFSSQIHNLGRADFRPKAGRHSWVWHECHGHYHSMDIFTHYDILTPN-GTKVAEGHKAS
huLor-2         LRFSSQIHNLGRADFRPKAGRHSWVWHECHGHYHSMDIFTHYDILTPN-GTKVAEGHKAS

                661                                                                720
LOX             FCLEDTSCDYGYHRRFACTAHT-QGLSPGCYDTYGADIDCQWIDITDVKPGNYILKVSVN
huLOL           FCLEDSTCDFGNLKRYACTSHT-QGLSPGCYDTYNADIDCQWIDITDVQPGNYILKVHVN
huLor           FCLEDTECEGDIQKNYECANFGDQGITMGCWDMYRHDIDCQWVDITDVPPGDYLFQVVIN
muLor-2         FCLEDTECQEDVSKRYECANFGEQGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVVIN
huLor-2         FCLEDTECQEDVSKRYECANFGEQGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVVIN

                721                                                                779
LOX             PSYLVPESDYTNNVVRCDIRYTGHHAYASGCTI----------------------SPY
huLOL           PKYIVLESDFTNNVVRCNIHYTGRYVSATNCKI----------------------VQS
huLor           PNFEVAESDYSNNIMKCRSRYDGHRIWMYNCHIGGSFSEETEKKFEHFSGLLNNQLSPQ
muLor-2         PNFEVAESDFTNNAMKCNCKYDGHRIWVHNCHIGDAFSEEANRRFERYPGQTSNQIV--
huLor-2         PNFEVAESDFTNNAMKCNCKYDGHRIWVHNCHIGDAFSEEANRRFERYPGQTSNQII--
```

Fig. 7B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WI-3580
7.5
WI-6130
23.5
h46a
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11.8
GATA72A05
8.9
WI-10237
11.0
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WI-10809
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5.0
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Fbh21967
16.7
GCT1B4
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10.0
D2S139
9.8
GATA26G08
12.5
GATA71D09
7.6
AFMB297YC5
10.0
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GATA88G05
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WI-6616
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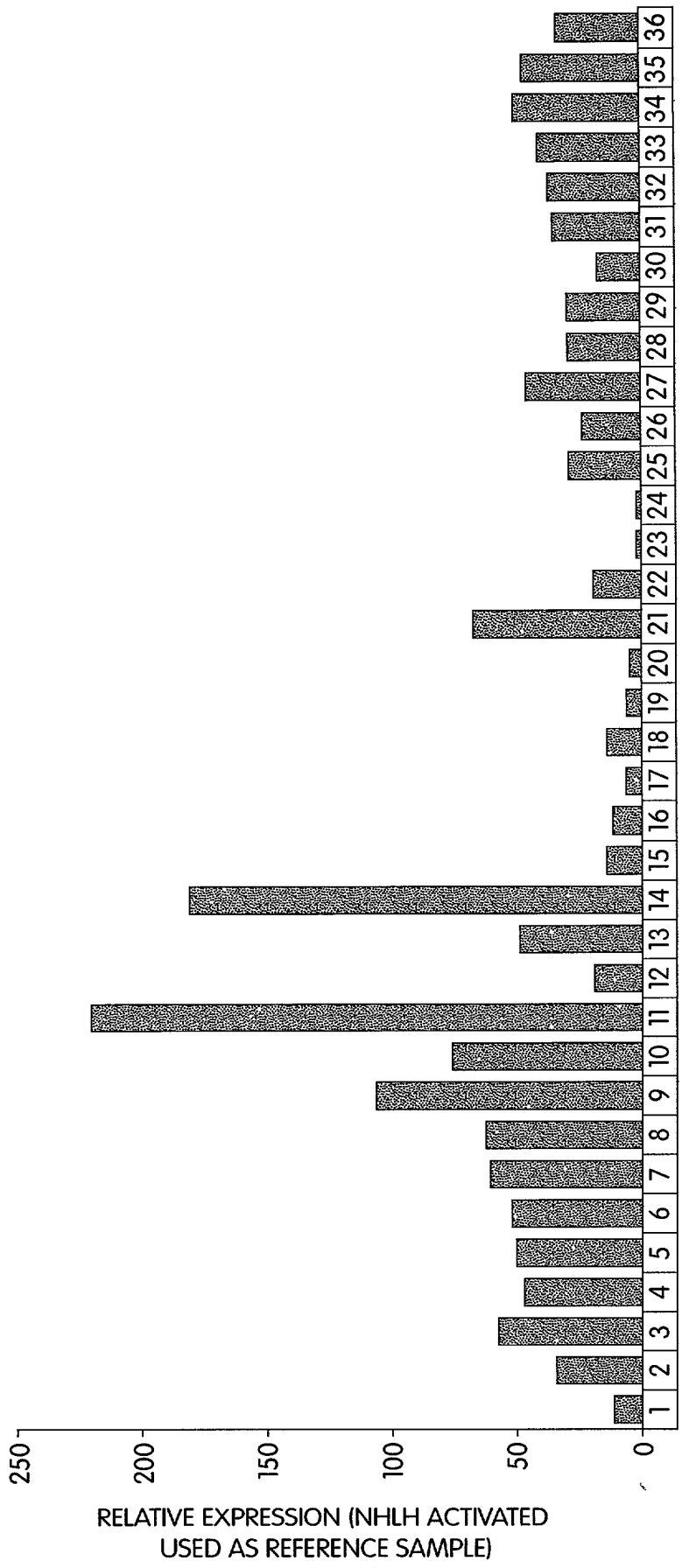
9.7
WI-4861
56.8
349365

Fig. 8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150
100
50
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1
2
3
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5
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7
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11
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16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
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32
33
34
35
36
RELATIVE EXPRESSION (NHLH ACTIVATED USED AS REFERENCE SAMPLE)
TISSUE TYPE

Fig. 9

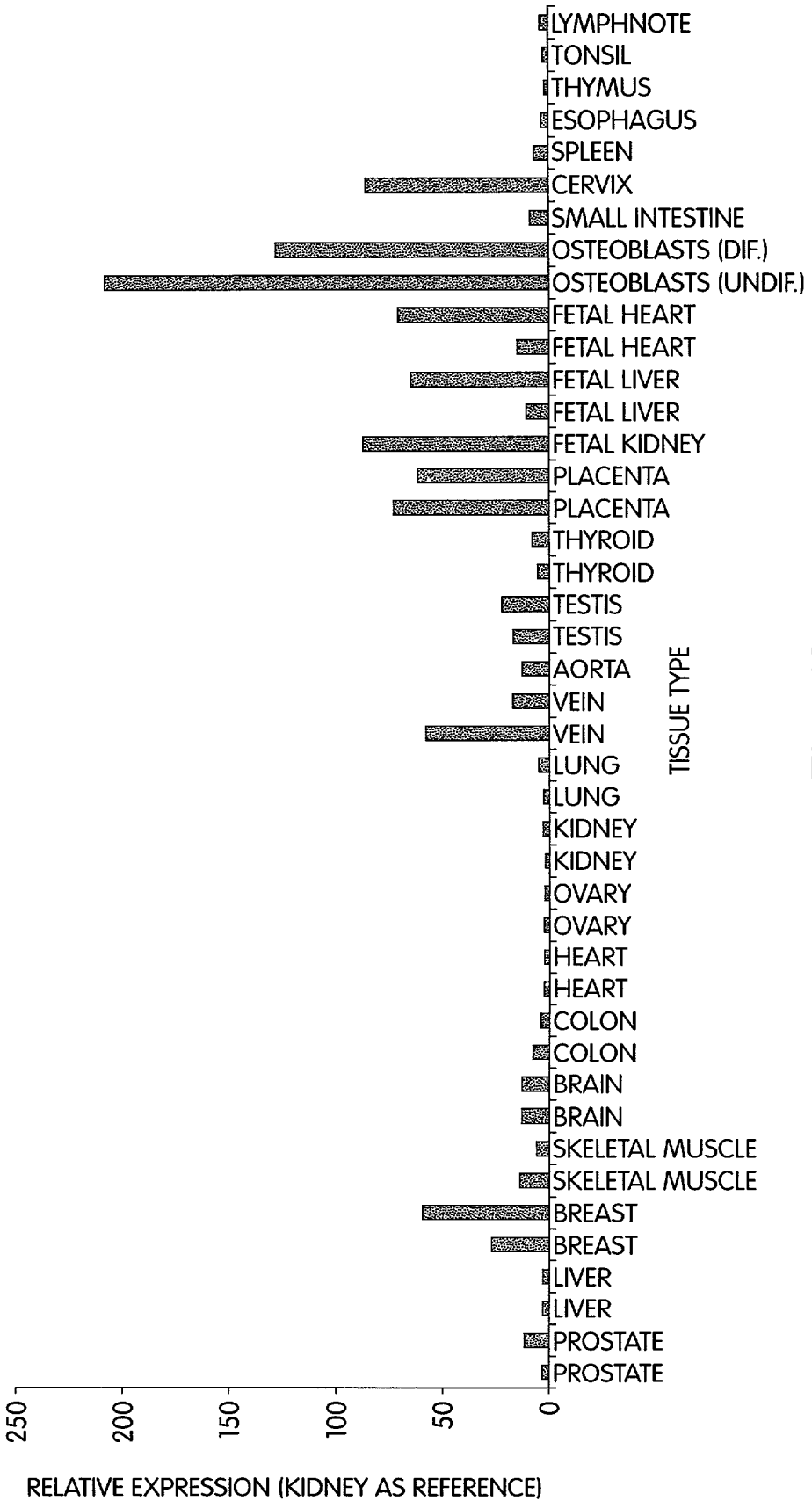

LYMPHNOTE
TONSIL
THYMUS
ESOPHAGUS
SPLEEN
CERVIX
SMALL INTESTINE
OSTEOBLASTS (DIF.)
OSTEOBLASTS (UNDIF.)
FETAL HEART
FETAL HEART
FETAL LIVER
FETAL LIVER
FETAL KIDNEY
PLACENTA
PLACENTA
THYROID
THYROID
TESTIS
TESTIS
AORTA
VEIN
VEIN
LUNG
LUNG
KIDNEY
KIDNEY
OVARY
OVARY
HEART
HEART
COLON
COLON
BRAIN
BRAIN
SKELETAL MUSCLE
SKELETAL MUSCLE
BREAST
BREAST
LIVER
LIVER
PROSTATE
PROSTATE
TISSUE TYPE
250
200
150
100
50
0
RELATIVE EXPRESSION (KIDNEY AS REFERENCE)

Fig. 10

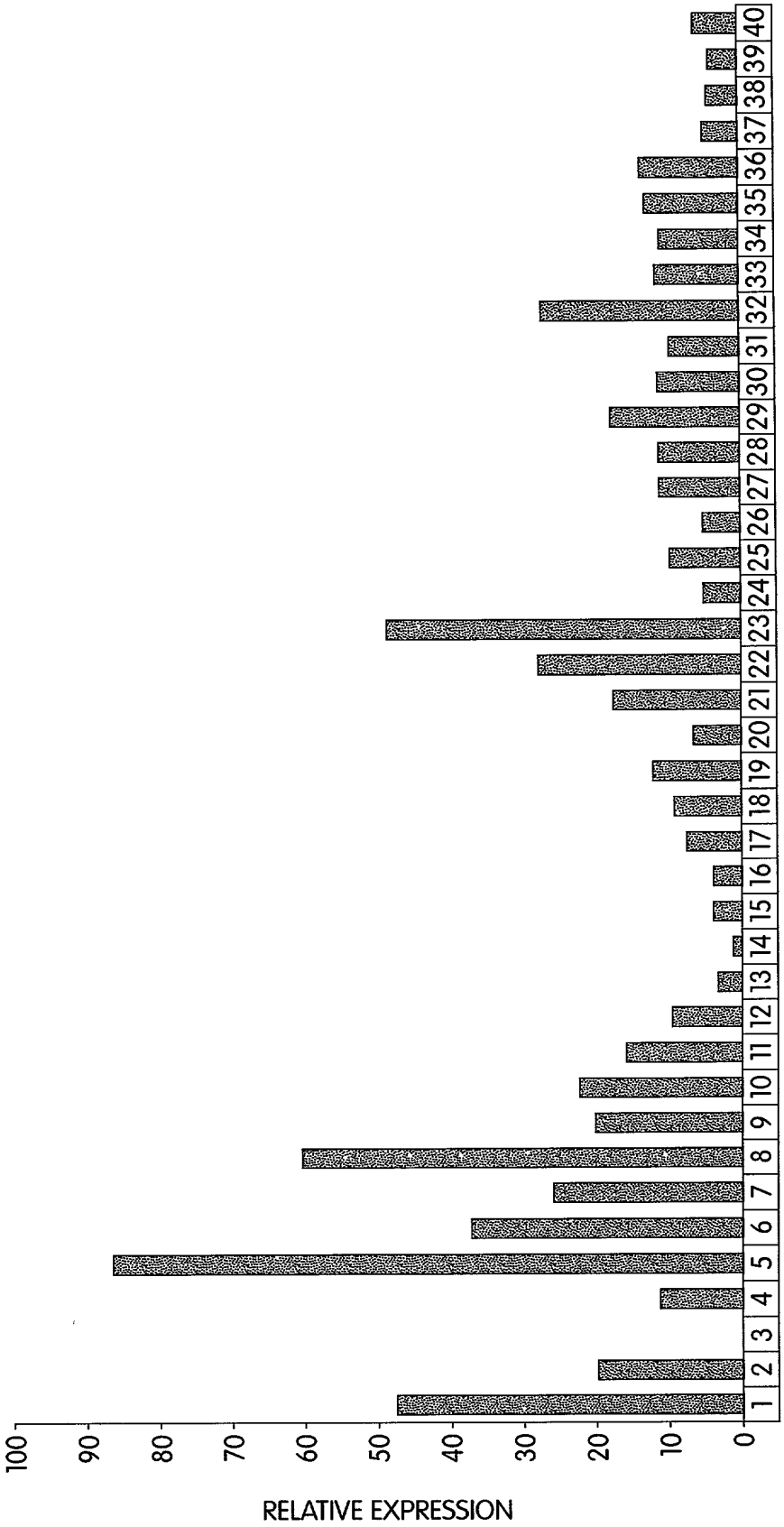

RELATIVE EXPRESSION
100
90
80
70
60
50
40
30
20
10
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40
TISSUE TYPE

Fig. 11

```
GAATTCGGCACGAGGGCCGGCACCCCCGCGCCACCCCAGCCTCAAACTGCAGTCCGGCGCCGCGGGGCAGGACAAGGGG 79

                                M   A   L   K   V   L   P   L   H   R   T   V   L  13
AAGGAATAAACACGTTTGGTGAGAGCC ATG GCA CTC AAG GTC CTA CCT CTA CAC AGG ACG GTG CTC 145

 F   A   A   I   L   F   L   L   H   L   A   C   K   V   S   C   E   T   G   D  33
TTC GCT GCC ATT CTC TTC CTA CTC CAC CTG GCA TGT AAA GTG AGT TGC GAA ACC GGA GAT 205

 C   R   Q   Q   E   F   K   D   R   S   G   N   C   V   L   C   K   Q   C   G  53
TGC AGG CAG CAG GAA TTC AAG GAT CGA TCT GGA AAC TGT GTC CTC TGC AAA CAG TGC GGA 265

 P   G   M   E   L   S   K   E   C   G   F   G   Y   G   E   D   A   Q   C   V  73
CCT GGC ATG GAG TTG TCC AAG GAA TGT GGC TTC GGC TAT GGG GAG GAT GCA CAG TGT GTG 325

 P   C   R   P   H   R   F   K   E   D   W   G   F   Q   K   C   K   P   C   A  93
CCC TGC AGG CCG CAC CGG TTC AAG GAA GAC TGG GGT TTC CAG AAG TGT AAG CCA TGT GCG 385

 D   C   A   L   V   N   R   F   Q   R   A   N   C   S   H   T   S   D   A   V 113
GAC TGT GCG CTG GTG AAC CGC TTT CAG AGG GCC AAC TGC TCA CAC ACC AGT GAT GCT GTC 445

 C   G   D   C   L   P   G   F   Y   R   K   T   K   L   V   G   F   Q   D   M 133
TGC GGG GAC TGC CTG CCA GGA TTT TAC CGG AAG ACC AAA CTG GTT GGT TTT CAA GAC ATG 505
```

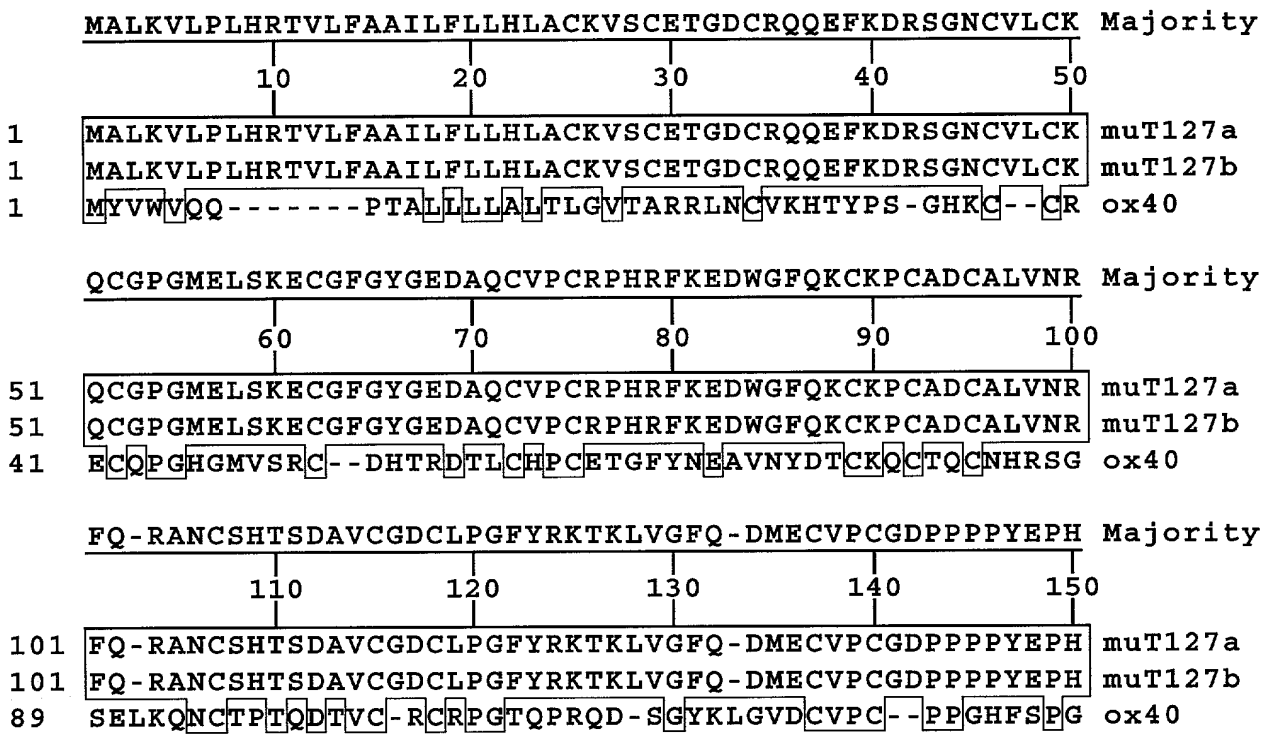
Fig. 12A

```
 E   C   V   P   C   G   D   P   P   P   P   Y   E   P   H   C   T   S   K   V   153
GAG TGT GTG CCC TGC GGA GAC CCA CCT CCT CCC TAC GAA CCA CAC TGT ACC AGC AAG GTG  565

 N   L   V   K   I   S   S   T   V   S   S   P   R   D   T   A   L   A   A   V   173
AAC CTT GTG AAG ATC TCC TCC ACC GTC TCC AGC CCT CGG GAC ACG GCG CTG GCT GCC GTC  625

 I   C   S   A   L   A   T   V   L   L   A   L   L   I   L   C   V   I   Y   C   193
ATC TGC AGT GCT CTG GCC ACG GTG CTG CTC GCC CTG CTC ATC CTG TGT GTC ATC TAC TGC  685

 K   R   Q   F   M   E   K   K   P   S   C   K   L   P   S   L   C   L   T   V   213
AAG AGG CAG TTC ATG GAG AAG AAA CCC AGC TGT AAG CTC CCA TCC CTC TGT CTC ACT GTG  745

 K   *                                                                           215
AAG TGA                                                                        751

GCTTGTTAGCATTGTCACCCAAGAGTTCTCAAGACACCTGGCTGAGACCTAAGACCTTTAGAGCATCAACAGCTACTTA  830

GAATACAAGATGCAGGAAAACGAGCCTCTTCAGGAATCTCAGGGCCTCCTAGGGATGCTGGCAAGGCTGTGATGTCTCA  909

AGGCTACCAGGAAAAAATAAAAGTTGTCTATACCCTAAAAAAAAAAAAAAAAAAAAAAAAACATGCGGCCGC        981
```

Fig. 12B

```
GAATTCGGCACGAGGGCGTTTGGCGCGGAAGTGCTACCAAGCTGCGGAAAGCGTGAGTCTGGAGCACAGCACTGGCGAG  79

                                  M   A   L   K   V   L   P   L   H   R   T   V    12
TAGCAGGAATAAACACGTTTGGTGAGAGCC ATG GCA CTC AAG GTC CTA CCT CTA CAC AGG ACG GTG  145

 L   F   A   A   I   L   F   L   L   H   L   A   C   K   V   S   C   E   T   G    32
CTC TTC GCT GCC ATT CTC TTC CTA CTC CAC CTG GCA TGT AAA GTG AGT TGC GAA ACC GGA  205

 D   C   R   Q   Q   E   F   K   D   R   S   G   N   C   V   L   C   K   Q   C    52
GAT TGC AGG CAG CAG GAA TTC AAG GAT CGA TCT GGA AAC TGT GTC CTC TGC AAA CAG TGC  265

 G   P   G   M   E   L   S   K   E   C   G   F   G   Y   G   E   D   A   Q   C    72
GGA CCT GGC ATG GAG TTG TCC AAG GAA TGT GGC TTC GGC TAT GGG GAG GAT GCA CAG TGT  325

 V   P   C   R   P   H   R   F   K   E   D   W   G   F   Q   K   C   K   P   C    92
GTG CCC TGC AGG CCG CAC CGG TTC AAG GAA GAC TGG GGT TTC CAG AAG TGT AAG CCA TGT  385

 A   D   C   A   L   V   N   R   F   Q   R   A   N   C   S   H   T   S   D   A   112
GCG GAC TGT GCG CTG GTG AAC CGC TTT CAG AGG GCC AAC TGC TCA CAC ACC AGT GAT GCT  445

 V   C   G   D   C   L   P   G   F   Y   R   K   T   K   L   V   G   F   Q   D   132
GTC TGC GGG GAC TGC CTG CCA GGA TTT TAC CGG AAG ACC AAA CTG GTT GGT TTT CAA GAC  505

 M   E   C   V   P   C   G   D   P   P   P   P   Y   E   P   H   C   E   *       151
ATG GAG TGT GTG CCC TGC GGA GAC CCA CCT CCT CCC TAC GAA CCA CAC TGT GAG TGA       562

TGTGCCAAGTGGCAGCAGACCTTTAAAAAAAAAAGAAAAAAAAACAAACAAAAACAAAAAAAAAAAAAAAAAAAAAA  641

ATTTCCGCGGCCGC                                                                 655
```

Fig. 13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10 20 30 40 50
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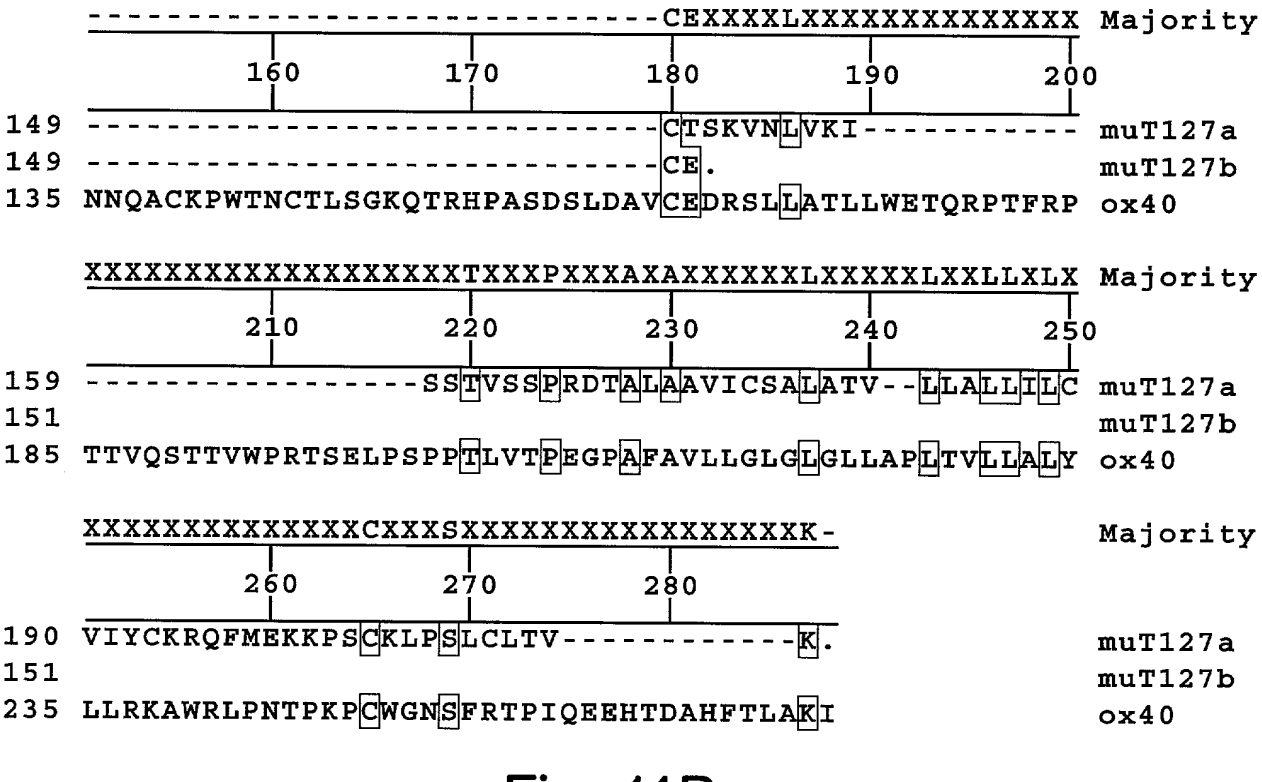
1 MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCK muT127b
1 MYVWVQQ-------PTALLLLALTLGVTARRLNCVKHTYPS-GHKC--CR ox40
QCGPGMELSKECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNR Majority
60 70 80 90 100
51 QCGPGMELSKECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNR muT127a
51 QCGPGMELSKECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNR muT127b
41 ECQPGHGMVSRC--DHTRDTLCHPCETGFYNEAVNYDTCKQCTQCNHRSG ox40
FQ-RANCSHTSDAVCGDCLPGFYRKTKLVGFQ-DMECVPCGDPPPPYEPH Majority
110 120 130 140 150
101 FQ-RANCSHTSDAVCGDCLPGFYRKTKLVGFQ-DMECVPCGDPPPPYEPH muT127a
101 FQ-RANCSHTSDAVCGDCLPGFYRKTKLVGFQ-DMECVPCGDPPPPYEPH muT127b
89 SELKQNCTPTQDTVC-RCRPGTQPRQD-SGYKLGVDCVPC--PPGHFSPG ox40

Fig. 14A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149 ----------CE. muT127b
135 NNQACKPWTNCTLSGKQTRHPASDSLDAVCEDRSLLATLLWETQRPTFRP ox40
XXXXXXXXXXXXXXXXXXTXXXPXXXAXAXXXXXXLXXXXXLXXLLXLX Majority
210 220 230 240 250
159 ----------SSTVSSPRDTALAAVICSALATV--LLALLLILC muT127a
151 muT127b
185 TTVQSTTVWPRTSELPSPPTLVTPEGPAFAVLLGLGLGLLAPLTVLLALY ox40
XXXXXXXXXXXXXCXXXSXXXXXXXXXXXXXXXXK- Majority
260 270 280
190 VIYCKRQFMEKKPSCKLPSLCLTV----------K. muT127a
151 muT127b
235 LLRKAWRLPNTPKPCWGNSFRTPIQEEHTDAHFTLAKI ox40

Fig. 14B

```
 FASTA searches a protein or DNA sequence data bank
 version 2.0u53 July, 1996
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

 inputs/nb589712.tmp :  215 aa
 > T127Atm473200aa: 215 aa
 vs  library
 searching inputs/nb782215.tmp library

    423 residues in     1 sequence
The best scores are:                                      initn init1 opt
 Patent Protein W70387 - (untitled)                         982 982  982

>> Patent Protein W70387 - (untitled)                        (423 aa)
initn:  982  init1:  982  opt:  982
Smith-Waterman score: 982;    85.7% identity in 203 aa overlap

               10        20        30        40        50        60

 T127A MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCKQCGPGMELSK

       X:::::  .  ..:. ...:  :.::::.:::::::::::.::::::: :.::::::::::

       MALKVLLEQEKTFFTLLVLLGYLSCKVTCETGDCRQQEFRDRSGNCVPCNQCGPGMELSK

               10        20        30        40        50        60
```

Fig. 15A

```
                70        80        90        100       110       120
T127A ECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNRFQRANCSHTSDAVCGDCLPG
      :::::::::::::: :: :::::::::::::: :::.:::::.:::: ::::.:::::::
      ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG
                70        80        90        100       110       120
               130       140       150       160       170       180
T127A FYRKTKLVGFQDMECVPCGDPPPPYEPHCTSKVNLVKISSTVSSPRDTALAAVICSALAT
      :::::::::::::::::::::::::::::::.:::::::.::.::::::::::::::::::
      FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT
               130       140       150       160       170       180
               190       200       210
T127A VLLALLILCVIYCKRQFMEKKPSCKLPSLCLTVKN
      ::::::::::::::::::::::X
      VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCLDPRQLHEYAHRACCQCRRD
               190       200       210       220       230       240
```

Fig. 15B

```
 FASTA searches a protein or DNA sequence data bank
 version 2.0u53 July, 1996
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

 inputs/nb504897.tmp :  981 aa
 > Atm472300: 981 aa
 vs  library
 searching inputs/nb658900.tmp library

   1496 residues in     1 sequences
The best scores are:                                      initn init1 opt
 Patent Nucleotide V33362 - (untitled)                     2575 2575 2861

>> Patent Nucleotide V33362 - (untitled)                    (1496 aa)
initn: 2575  init1: 2575  opt: 2861
Smith-Waterman score: 2888;    70.6% identity in 922 aa overlap

            40        50        60        70        80        90

 Atm47 CCCCAGCCTCAAACTGCAGTCCGGCGCCGCGGGGCAGGACAAGGGGAAGGAATAAACACG

                                      X:..:. .. :      :. :::::: ::.

                                    GGGAACGTAGAACTCTCCAACAATAAATACA

                                             10        20        30
```

Fig. 16A

```
          100        110        120        130        140        150
Atm47 TTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACGGTGCTCTTCGCTGC
      :::::.:.:::.  ::::::. : ::.:: :::: . .::: ..:: .. : : :::.::
      TTTGATAAGAAAGATGGCTTTAAAAGTGCTACTAGAACAAGAGAAAACGTTTTTCACTCT
            40         50         60         70         80         90
           160        170        180        190        200        210
Atm47 CATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACCGGAGATTGCAGGCA
       .:. : :: :::  : :  :: :::::::::::: ::: ::::: ::::: :: ::.::
      TTTAGTATTACTAGGCTATTTGTCATGTAAAGTGACTTGTGAAACAGGAGACTGTAGACA
           100        110        120        130        140        150
```

Fig. 16B

```
          220        230        240        250        260        270
Atm47 GCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGCGGACCTGGCAT
      :::.:::::::.:::::::.:::::::::::::::: : :::::: ::::: ::.::.:::::
      GCAAGAATTCAGGGATCGGTCTGGAAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCAT
           160        170        180        190        200        210
          280        290        300        310        320        330
Atm47 GGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTGTGCCCTGCAG
      ::::::::: :::::::::::::::::::::::::::::::::::::::::: : ::: :
      GGAGTTGTCTAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTGTGACGTGCCG
           220        230        240        250        260        270
```

Fig. 16C

```
          340        350        360        370        380        390
Atm47 GCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCATGTGCGGACTGTGC
      :: :::: ::::::::::.:::::::: :::::::.:: ::::: ::: ::::::: ::
      GCTGCACAGGTTCAAGGAGGACTGGGGCTTCCAGAAATGCAAGCCCTGTCTGGACTGCGC
           280        290        300        310        320        330
          400        410        420        430        440        450
Atm47 GCTGGTGAACCGCTTTCAGAGGGCCAACTGCTCACACACCAGTGATGCTGTCTGCGGGGA
      . ::::::::::::::::::.::: :: :: ::: :::::::::::: .::::::::::
      AGTGGTGAACCGCTTTCAGAAGGCAAATTGTTCAGCCACCAGTGATGCCGTCTGCGGGGA
           340        350        360        370        380        390
```

Fig. 16D

```
          460        470        480        490        500        510
Atm47 CTGCCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAAGACATGGAGTGTGT
      :::: ::::::::::::  ::::::: ::::: :: :: ::::::::::::::::::::
      CTGCTTGCCAGGATTTTATAGGAAGACGAAACTTGTCGGCTTTCAAGACATGGAGTGTGT
           400        410        420        430        440        450
          520        530        540        550        560        570
Atm47 GCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTACCAGCAAGGTGAACCTTGT
      ::: :: :::::::::.:::::::: :::::::::.::::::.:::::::::: ::::: ::
      GCCTTGTGGAGACCCTCCTCCTCCTTACGAACCGCACTGTGCCAGCAAGGTCAACCTCGT
           460        470        480        490        500        510
```

Fig. 16E

```
          580        590        600        610        620        630
Atm47 GAAGATCTCCTCCACCGTCTCCAGCCCTCGGGACACGGCGCTGGCTGCCGTCATCTGCAG
      ::::::: : ::::: : ::::::::::.:::::::::::::::::::::::::: ::::::::
      GAAGATCGCGTCCACGGCCTCCAGCCCACGGGACACGGCGCTGGCTGCCGTTATCTGCAG
            520        530        540        550        560        570
          640        650        660        670        680        690
Atm47 TGCTCTGGCCACGGTGCTGCTCGCCCTGCTCATCCTGTGTGTCATCTACTGCAAGAGGCA
       :::::::::::: :: ::::: :::::::::::::: :::::::::: :: ::::::.::
      CGCTCTGGCCACCGTCCTGCTGGCCCTGCTCATCCCCTGTGTCATCTATTGTAAGAGACA
            580        590        600        610        620        630
```

Fig. 16F

```
          700        710        720        730        740        750
Atm47 GTTCATGGAGAAGAAACCCAGCTGTAAGCTCCCATCCCTCTGTCTCACTGTGAAGTGAGC
      ::: :::::::::::::::::::: .  :: : .:: :.  :.:. .:.::. :. : ::
      GTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTCACA-GGACATTCAGTACAACG-GC
           640        650        660        670        680
          760        770        780        790        800        810
Atm47 TTGTTAGCATT-GTCACCCAAGAGTTCTCAAGACACCT-GGCTGAGACCTAAGA-CCTTT
      :  : :::. : :: .:  .: ::. :^:v.  :.::. :. :..: ::. ::: :::
      TC-TGAGCTGTCGTGTCTTGACAGACCTCAG--CTCCACGAATATGCCCACAGAGCCT--
    690        700        710         720        730        740
```

Fig. 16G

```
            820        830        840        850        860        870
Atm47 AGAGCATCAACAGCTACTTAGAATACAAGATGCAGGAAAACGAGCCTCTTCAGGAATCTC
      ::. : : .:: .:  .::   :. ..:::::.  ..::.:::  : : : .. :::
      ---GCTGCCAGTGCCGCCGTGA---CTCAGTGCAGACCTGCGGGCCGGTGC-GCTTGCTC
         750        760          770        780        790

            880        890        900        910        920        930
Atm47 AGGGCCTCCTAGGGATGCTGGCAAGGCTGTGATGTCTCAAGGCTACCAGGAAAAAATAAA
       : :::..: : :: ::. .:::: :: .: : ::: : ::.: .: . .:...
      C---CATCCATGTGCTG-TGAGGAGGCC-TGCAGCCCCAA--C--CCGGCGACTCTTGGT
         800        810        820        830          840
```

Fig. 16H

```
                940        950        960        970         980

Atm47 AGTTGTCTATACCCTAAAAAAAAAAAAAAAAAAAAAAAAAACATGC--GGCCGC

      .:: :  :. :  ::. :.  :.. .. :.. ::.::: .:: ::  .::::

      TGTGGGGTGCATTCTGCAGCCAGTCTTCAGGCAAGAAACGCAGGCCCAGCCGGGGAGATG

     850        860        870        880        890        900

      GTGCCGACTTTCTTCGGATCCCTCACGCAGTCCATCTGTGGCGAGTTTTCAGATGCCTGG

     910        920        930        940        950        960
```

Fig. 16l

```
GAATTCGGAACGAGGGGAACCTAATTCTCCTGAGGCTGAGGGAGGGTGGAGGGTCTCAAGGCAACGCTGGCCCCACGAC   79

GGAGTGCCAGGAGCACTAACAGTACCCTTAGCTTGCTTTCCTCCTCCCTCCTTTTTATTTTCAAGTTCCTTTTTATTTC   158

TCCTTGCGTAACAACCTTCTTCCCTTCTGCACCACTGCCCGTACCCTTACCCGCCCCGCCACCTCCTTGCTACCCCACT   237

                                        M  P  A  S  S  P  F  L  L  A  P    11
CTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTC ATG CCA GCC TCA TCT CCT TTC TTG CTA GCC CCC   305

 K  G  P  P  G  N  M  G  G  P  V  R  E  P  A  L  S  V  A  L    31
AAA GGG CCT CCA GGC AAC ATG GGG GGC CCA GTC AGA GAG CCG GCA CTC TCA GTT GCC CTC   365

 W  L  S  W  G  A  A  L  G  A  V  A  C  A  M  A  L  L  T  Q    51
TGG TTG AGT TGG GGG GCA GCT CTG GGG GCC GTG GCT TGT GCC ATG GCT CTG CTG ACC CAA   425

 Q  T  E  L  Q  S  L  R  R  E  V  S  R  L  Q  G  T  G  G  P    71
CAA ACA GAG CTG CAG AGC CTC AGG AGA GAG GTG AGC CGG CTG CAG GGG ACA GGA GGC CCC   485

 S  Q  N  G  E  G  Y  P  W  Q  S  L  P  E  Q  S  S  D  A  L    91
TCC CAG AAT GGG GAA GGG TAT CCC TGG CAG AGT CTC CCG GAG CAG AGT TCC GAT GCC CTG   545

 E  A  W  E  N  G  E  R  S  R  K  R  R  A  V  L  T  Q  K  Q   111
GAA GCC TGG GAG AAT GGG GAG AGA TCC CGG AAA AGG AGA GCA GTG CTC ACC CAA AAA CAG   605

 K  K  Q  H  S  V  L  H  L  V  P  I  N  A  T  S  K  D  D  S   131
AAG AAG CAG CAC TCT GTC CTG CAC CTG GTT CCC ATT AAC GCC ACC TCC AAG GAT GAC TCC   665

 D  V  T  E  V  M  W  Q  P  A  L  R  R  G  R  G  L  Q  A  Q   151
GAT GTG ACA GAG GTG ATG TGG CAA CCA GCT CTT AGG CGT GGG AGA GGC CTA CAG GCC CAA   725

 G  Y  G  V  R  I  Q  D  A  G  V  Y  L  L  Y  S  Q  V  L  F   171
GGA TAT GGT GTC CGA ATC CAG GAT GCT GGA GTT TAT CTG CTG TAT AGC CAG GTC CTG TTT   785

 Q  D  V  T  F  T  M  G  Q  V  V  S  R  E  G  Q  G  R  Q  E   191
CAA GAC GTG ACT TTC ACC ATG GGT CAG GTG GTG TCT CGA GAA GGC CAA GGA AGG CAG GAG   845

 T  L  F  R  C  I  R  S  M  P  S  H  P  D  R  A  Y  N  S  C   211
ACT CTA TTC CGA TGT ATA AGA AGT ATG CCC TCC CAC CCG GAC CGG GCC TAC AAC AGC TGC   905

 Y  S  A  G  V  F  H  L  H  Q  G  D  I  L  S  V  I  I  P  R   231
TAT AGC GCA GGT GTC TTC CAT TTA CAC CAA GGG GAT ATT CTG AGT GTC ATA ATT CCC CGG   965

 A  R  A  K  L  N  L  S  P  H  G  T  F  L  G  F  V  K  L  *   251
GCA AGG GCG AAA CTT AAC CTC TCT CCA CAT GGA ACC TTC CTG GGG TTT GTG AAA CTG TGA  1025

TTGTGTTATAAAAAGTGGCTCCCAGCTTGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAAGAGCTGAGTATATAA  1104

AGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCCTGGGTTTGGCTCCCCGTTCCTCACTTTTCCCTTTTCATTCCCAC  1183

CCCCTAGACTTTGATTTTACGGATATCTTGCTTCTGTTCCCCATGGAGCTCCGAATTCTTGCGTGTGTGTAGATGAGGG  1262

GCGGGGGACGGGCGCCAGGCATTGTTCAGACCTGGTCGGGGCCCACTGGAAGCATCCAGAACAGCACCACCATCTAGCG  1341

GCCGC                                                                              1346
```

Fig. 17

```
T118 pileup.msf  MSF: 286
1913 ..
Name: Trash  Len: 286  Check:  7625   Weight: 1.00
Name: TNF    Len: 286  Check:  5421   Weight: 1.00
Name: tweak  Len: 286  Check:  8867   Weight: 1.00
//
       1                                                          60
TRASH  MPASSPFL...LAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQS
  TNF  MSTESMIRDVELAEEALPKKTGGP...QGSRRCLFLSLFSFL.........IVAGATTLFC
tweak  MAARR.........SQRRRGRRGEPGTALLVPLALGLGL.....ALAC.LGLLLAVVSLGS

       61                                                         120
TRASH  LRREVSRLQ.GTGGPSQNGEGYPWQ.SLPEQSSDALEAWENGERSRKRRAVLTQKQKKQH
  TNF  L......LHFGVIGPQR..EEFPRDLSLISPLAQAV.......RSSSRTP.......SDK
tweak  .RASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARR

       121                                                        180
TRASH  SV.....LHLVPINATSKDDSDVTEVMWQPALRRGRGLQAQGYGVR.....IQDAGVYLL
  TNF  PV.....AHVVANPQAE......GQLQWLN..RRANALLANGVELRDNQLVVPSEGLYLI
tweak  AIAAHYEVHPRPGQDGAQAGVDGTVSGWEEA..RINSSSPLRYNRQIGEFIVTRAGLYYL

       181                                                        240
TRASH  YSQVLFQDVTFTMGQVVSREGQGRQETLFR.............CIRSMPSHPDRA....
  TNF  YSQVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLL..SAIKSPCQRETPEGAEAK..PW
tweak  YCQVHFDEG.................KAVYL.KLDLLVDGVLALRCLEEFSATAASSLGPQ

       241                                                    286
TRASH  YNSCYSAGVFHLHQGDILSV.IIPRARAKLNLSPHG.TFLGFVKL.
  TNF  YEPIYLGGVFQLEKGDRLSA.EINRPDY.LDFAESGQVYFGIIAL.
tweak  LRLCQVSGLLALRPGSSLRIRTLPWAHLK...AAPFLTYFGLFQVH
```

Fig. 18

```
GTCGACCCAC GCGTCCGGCA GGATGTTTGC AGTGTCGCGC CCAGGGCTCT GAGACTGAGC      60

CTGCCATCCA CTCGCACGCC TTTCTTTCAG GGCTTTTCGG CTGTTGGCTA CACTGATGTG     120

ACCCCCCTCC CTTTTTGGA ATG ATG GGG ATC TTT TTG GTG TAT GTT GGA TTT      172
                     Met Met Gly Ile Phe Leu Val Tyr Val Gly Phe
                       1               5                  10

GTT TTC TTT TCC GTT TTA TAT GTA CAA CAA GGG CTT TCT TCT CAA GCA      220
Val Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala
             15                  20                  25

AAA TTT ACC GAG TTT CCG CGG AAC GTG ACG GCG ACC GAG GGG CAG AAT      268
Lys Phe Thr Glu Phe Pro Arg Asn Val Thr Ala Thr Glu Gly Gln Asn
         30                  35                  40

GTG GAG ATG TCC TGC GCC TTC CAG AGC GGC TCC GCC TCG GTG TAT CTG      316
Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu
     45                  50                  55

GAG ATC CAA TGG TGG TTC CTG CGG GGG CCG GAG GAC CTG GAT CCC GGG      364
Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Asp Pro Gly
 60                  65                  70                  75

GCC GAG GGG GCC GGC GCG CAG GTG GAG CTC TTG CCC GAC AGA GAC CCG      412
Ala Glu Gly Ala Gly Ala Gln Val Glu Leu Leu Pro Asp Arg Asp Pro
                 80                  85                  90

GAC AGC GAC GGG ACC AAG ATC AGC ACA GTG AAA GTC CAA GGC AAT GAC      460
Asp Ser Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly Asn Asp
             95                  100                 105

ATC TCC CAC AAG CTT CAG ATT TCC AAA GTG AGG AAA AAG GAT GAA GGC      508
Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp Glu Gly
        110                 115                 120

TTA TAT GAG TGC AGG GTG ACT GAT GCC AAC TAC GGG GAG CTT CAG GAA      556
Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu
    125                 130                 135

CAC AAG GCC CAG GCC TAT CTG AAA GTC AAT GCC AAC AGC CAT GCC CGC      604
His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His Ala Arg
140                 145                 150                 155

AGA ATG CAG GCC TTC GAA GCC TCG CCC ATG TGG CTG CAG GAT ATG AAG      652
Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp Met Lys
                160                 165                 170

CCC CGC AAG AAC GTC TCC GCA GCC ATC CCC AGC AGC ATC CAT GGC TCT      700
Pro Arg Lys Asn Val Ser Ala Ala Ile Pro Ser Ser Ile His Gly Ser
            175                 180                 185

GCC AAC CAA CGA ACG CAC TCC ACC TCC AGC CCT CAA GTG GTA GCC AAA      748
Ala Asn Gln Arg Thr His Ser Thr Ser Ser Pro Gln Val Val Ala Lys
        190                 195                 200
```

Fig. 19A

```
ATC CCC AAA CAA AGT CCA CAA TCA GGT ATG GAA ACC CAT TTC GAG CCT    796
Ile Pro Lys Gln Ser Pro Gln Ser Gly Met Glu Thr His Phe Glu Pro
    205                 210                 215

TTT ATT TTA CCA CTC ACA AAC GCT CCA CAG AAA GGT CAG TCG TAT AGA    844
Phe Ile Leu Pro Leu Thr Asn Ala Pro Gln Lys Gly Gln Ser Tyr Arg
220                 225                 230                 235

GTA GAC AGA TTT ATG AAT GGT GAT TTT TAAAATCGGA GACCTAGTTC          891
Val Asp Arg Phe Met Asn Gly Asp Phe
                240

AGTGCAAGTG ATTATGAGAG GTGAGCACTG AGCCTGCACC AATTCACTCA GAGCTCAAAG  951

CATGTGGGTG CACCCCGTCA GTCCCCTAGT GGTGCTTCAT TTCCAGGGCA TCTGAGAGCT 1011

GGACTCTGGT TTTTATCCTT TCTGTATTTA CACATTATAA GAACAATAAA TCATGTAATG 1071

TTGGTTACAT TACAAAAAAA AAAAAAAAAA AAAAAAAAGG GCGGCCGC              1119
```

Fig. 19B

SUBSTITUTE SHEET (RULE 26)

```
CACGCGTCCG CAGCCAGCCG GCGGCGGAGA CACTTCACGG CGTGGCAACC CGGGTCTGTG    60

CCTTGAAGCC TCCGGATCGC AGCCAGCTCG GTCCATCCCT CACTAGTCGC AATCCCCTGT   120

GTCCAAGCTA CTCTTTGCTA TGAGCGGCAG CATGCGTGCA GTATCGCGCC CCAGGCTCTG   180

AGAGCAGCCT GCGGACACGC TTGCCTATCT GTCTTTTTAG GTTTTGGGGC TCTGGGCTAC   240

ACGGATGTGC CCCACTCCCT TGGCATG ATG GGG ATC TTT TTG GCG TCT GTT        291
                              Met Gly Ile Phe Leu Ala Ser Val
                                1               5

GGA TTT ATG TTC TTT TCC GTG TTA TAT GTA CAA CAA GGG CTT TCT TCT      339
Gly Phe Met Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu Ser Ser
     10                  15                  20

CAA GCA AAA TTT ACC GAG TTG CCG AGA AAT GTG ACT GCT ACC GAA GGG      387
Gln Ala Lys Phe Thr Glu Leu Pro Arg Asn Val Thr Ala Thr Glu Gly
 25                  30                  35                  40

CAA AAT GTG GAG ATG TCC TGT GCT TTC CAA AGC GGC TCT GCT TCA GTG      435
Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val
                 45                  50                  55

TAC CTG GAG ATC CAG TGG TGG TTC CTT CGG GGG CCA GAG GAC CTG GAG      483
Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Glu
             60                  65                  70

CAA GGC ACG GAG GCT GCA GGC TCG CAG GTG GAG CTC TTA CCC GAC AGA      531
Gln Gly Thr Glu Ala Ala Gly Ser Gln Val Glu Leu Leu Pro Asp Arg
         75                  80                  85

GAC CCG GAC AAC GAT GGG ACC AAG ATT AGT ACA GTG AAA GTC CAA GGC      579
Asp Pro Asp Asn Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly
     90                  95                 100

AAT GAT ATC TCC CAC AAG CTT CAG ATA TCC AAA GTG AGA AAA AAG GAT      627
Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp
105                 110                 115                 120

GAA GGT TTA TAC GAG TGC AGG GTG ACT GAC GCT AAC TAC GGG GAG CTT      675
Glu Gly Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu
                125                 130                 135

CAG GAA CAC AAG GCC CAG GCC TAT CTG AAA GTC AAT GCC AAC AGC CAT      723
Gln Glu His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His
            140                 145                 150

GCT CGG AGG ATG CAG GCC TTT GAA GCC TCA CCT ATG TGG CTG CAA GAC      771
Ala Arg Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp
        155                 160                 165

ACG AAG CCT CGA AAG AAC GCA TCA TCG GTG GTT CCC AGC AGC GTC CAC      819
Thr Lys Pro Arg Lys Asn Ala Ser Ser Val Val Pro Ser Ser Val His
    170                 175                 180
```

Fig. 20A

```
AAC TCT GCC AAC CAA CGA ATG CAC TCC ACC TCC AGC CCT CAA GCG GTA      867
Asn Ser Ala Asn Gln Arg Met His Ser Thr Ser Ser Pro Gln Ala Val
185                 190                 195                 200

GCC AAA ATC CCC AAG CAA AGT CCA CAA TCA GCA AAG AGC AAA TCG CCT      915
Ala Lys Ile Pro Lys Gln Ser Pro Gln Ser Ala Lys Ser Lys Ser Pro
                205                 210                 215

GTA AAA TCT ACG GAG CGG ACA GCA AAG TTG ACC CTA TAC TCC AAG CAC      963
Val Lys Ser Thr Glu Arg Thr Ala Lys Leu Thr Leu Tyr Ser Lys His
            220                 225                 230

CAT TCT GCA CCC CTG TAC TCT AGT TAT CTA CAC AAG GAG CAT CAG CTT     1011
His Ser Ala Pro Leu Tyr Ser Ser Tyr Leu His Lys Glu His Gln Leu
        235                 240                 245

CCG GAA GCA TAAGTGAAGA CACTGTCACA CGCTTTATTG ATAATATTTT             1060
Pro Glu Ala
    250

CTTTGGGAAG TTGCTGATCT TTTATTTCAA GAGAATTAAT GGGAAGAGAT AGGACATTTT   1120

CCAATTACAA GACCAATTTT TTTCCTTTTA TTTCAACAAA TAAAACCTGC ATTTCACTGA   1180

CTGCTCAGGA GTTGGCCTGA ATGACATCAG TATACTAAAT ATTTCCATGG ATTCCACCAA   1240

TTTCCTAACG AGGGACACCT AATCTTCAAG AAGCAAACAA AGATGGAAAA CCTAAGAACC   1300

ACAAACTGTC TCATACAGCA CCCCAGCTGA GGAACAAAAC AAATAGCTAA ATGCTGACCA   1360

TGGCAAATCA ACATCAGACA ACTTTATTTT ACATATGGAA TAATCAAAGA AAGTTTTTTT   1420

TTTACTTCCT TTTTGCCCCC TGGAATTTAT CTTGGAGTTT CCCTTTTTTC CTTGATTGCC   1480

GTTTTCGTTC AATGGTAGCA AGTGCCAATT ATGGCCAATC CTTGTCAATC CTGGAAGGTT   1540

TATATTCATA TACATTGAGT GTGGTATATA TCAATGTATT TTAATTCATT TGGCAATTTC   1600

TGTATAGGCA AACCTGGCAA ATTCTGTAAA TTGCTTATAG TATGTGTGAT ATGACTTCAA   1660

GGTAGATAGG CTATGATGCT CATGCAAGCT GACTTTCTTC ATTCTATATA CAAATATATT   1720

CATGAGCATA TATTAGGCCA CCAACTTCTT TTCCTAAAGA ATTATTTTTC ATTTGTACCT   1780

CATGTATTTT GTGAATTTTG TAGTATATTT CTCTGTTCCA CTAGTTTGAC CGCTACAGTT   1840

TGTCTCTGTT GTCCTCTACT TCCTTCTGGA AAAATTTAAA ATTGTGTATG TCTCTGATAA   1900

ATGAATTAAT TTTGTTGTGT GTATGCTATG TTGGAATTTG CTGTGTTCTT TTAAACATGT   1960

ATTTATTAAG GTTTGGGGAT CTTGAGTTGA GTCTGAAGAA TGCACACCTG GTTTTTGACA   2020

GAGTTCCTCA TGTTACCAAT ATTCTATCTC AGAGAAAGAA AGACACCAAG TGGGAAAACT   2080

AAGAAGACAT TTTGACTTCC CAAGATCCTG GAAGAGCACT TCACACTCTG ACTAAATAAT   2140

GTTGCTTTTT TTGTTCTTCA AGACTTTTTT GTAGCTTTGT CTTTCTGTTA GTTGCTGCTA   2200

ATTATATTTT AATGTCTACT AATTAAAAAT TAAAATGTGA TTGTTGGCTG AATACAATAT   2260
```

Fig. 20B

Replacement Sheet

GCAAATGACT GCAAAGCCCA TACTGAAGAA AATAGATGTT TAATCTTCAC TCAATAATTA 2320

TAATTTTAAA TAGTTCATCA TTATTTTTTG ACCTTATGAT ATTTTGTTTA GACCTGTTCT 2380

AATTACATCT TTCTCTGGCA AAGAAAGATA GAACAATCAA TACATTCCCT CTTACAGTAT 2440

GGAATGGTTG TGGCTTAAGA AAGAATGCAT CCAGATGGTC TTCCAGAGAG ATTATTTTAT 2500

TTTCATTATA AAACCAGAAA CCATATATGT AGGAATGGTT CATTCCTAAT GTAAGGCCAT 2560

AAATTGTAGC TTGAAGGCAA GGAATACATT TGTTTTTTTA TGGTAAAGGA CTGGCCTCTG 2620

ACATGCACTT ATAAGCAATG TGAATATTTT CATAATATGC TTGACATTCT CCTTTAACAA 2680

ATATTGTTTT ATGGTAAATC TTTCCTTGCC ATTTTTCTTC TTTCATTTGA TTCATTATTT 2740

CATTCTAATG AAGAAAATAA AGGTTTAATT ATGATACTTT ATTAACATAC AAATGTATTT 2800

TCTTTCTAAG TTAAATATCT GAAAGTTGTA TAAAATGATG GTAGAGAAAT ATTACTCATT 2860

CGGTTTCTTT GAGCTTTAAG AATCCCATAC ATTGCAGTAT ATATTAGAAT ACTGATTTAA 2920

CATCAAACTG GGGGGGAAAA TCATGTATTA TACTTTTACT CAATGTCTAG GTAATGGATT 2980

CAGCTAATTT TACAGCAAGC CAAATGTGTA CCCGTATCAG TAATGTTCAC CATGCTTGTA 3040

ATAAAAGGGC ATATGCTAGT TTTGGAAGAA TGCTCATTAG ATTCATTGTA TCAGTGTCCA 3100

AAATAATAAA GACCTGTTTA TCACTGTGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3160

AAAAAAAAAA AAAAAAAAAA AAAAAAGGGC GGCCGC 3196

Fig. 20C

```
>_ hT122                                                    244 aa vs.
>_ mT122                                                    251 aa
scoring matrix: , gap penalties: -12/-2
77.4% identity;          Global alignment score: 1236

                10        20        30        40       *50        60
hT122    MMGIFLVYVGFVFFSVLYVQQGLSSQAKFTEFPRNVTATEGQNVEMSCAFQSGSASVYLE
         : ::::. :::.:::::::::::::::::::::.:::::::::::::::::::::::::
mT122    M-GIFLASVGFMFFSVLYVQQGLSSQAKFTELPRNVTATEGQNVEMSCAFQSGSASVYLE
                 10        20        30        40       * 50

                70        80        90       100       110       120
hT122    IQWWFLRGPEDLDPGAEGAGAQVELLPDRDPDSDGTKISTVKVQGNDISHKLQISKVRKK
         :::::::::::::. :.:.::.:::::::::::.:::::::::::::::::::::::::
mT122    IQWWFLRGPEDLEQGTEAAGSQVELLPDRDPDNDGTKISTVKVQGNDISHKLQISKVRKK
        60        70        80        90       100       110

               *130       140       150       160       170       180
hT122    DEGLYECRVTDANYGELQEHKAQAYLKVNANSHARRMQAFEASPMWLQDMKPRKNVSAAI
         :::::::::::::::::::::::::::::::::::::::::::::::: ::::::.:...
mT122    DEGLYECRVTDANYGELQEHKAQAYLKVNANSHARRMQAFEASPMWLQDTKPRKNASSVV
       120     * 130       140       150       160       170

                190       200       210            220       230
hT122    PSSIHGSANQRTHSTSSPQVVAKIPKQSPQSG-----METHFEPFILPLTNAPQKG---Q
         :::.:.:::::: :::::::.:::::::::::.     ...  .   : : .  ...   .
mT122    PSSVHNSANQRMHSTSSPQAVAKIPKQSPQSAKSKSPVKSTERTAKLTLYSKHHSAPLYS
       180       190       200       210       220       230

             240
hT122    SYRVDRFMNGDF
         ::   . .  .
mT122    SYLHKEHQLPEA
       240       250

 Elapsed time:   0:00:00
```

Fig. 21

```
GTCGACCCACGCGTCCGGAGCCCGGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGG  79

GCCCGACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCGGCTCCCTGCGCCGCCGCCGCCTCCCGGGACAGAA 158

   M   C   S   R   V   P   L   L   L   P   L   L   L   L   L   A   L   G   P      19
G ATG TGC TCC AGG GTC CCT CTG CTG CTG CCG CTG CTC CTG CTA CTG GCC CTG GGG CCT     216

 G   V   Q   G   C   P   S   G   C   Q   C   S   Q   P   Q   T   V   F   C   T    39
GGG GTG CAG GGC TGC CCA TCC GGC TGC CAG TGC AGC CAG CCA CAG ACA GTC TTC TGC ACT   276

 A   R   Q   G   T   T   V   P   R   D   V   P   P   D   T   V   G   L   Y   V    59
GCC CGC CAG GGG ACC ACG GTG CCC CGA GAC GTG CCA CCC GAC ACG GTG GGG CTG TAC GTC   336

 F   E   N   G   I   T   M   L   D   A   G   S   F   A   G   L   P   G   L   Q    79
TTT GAG AAC GGC ATC ACC ATG CTC GAC GCA GGC AGC TTT GCC GGC CTG CCG GGC CTG CAG   396

 L   L   D   L   S   Q   N   Q   I   A   S   L   P   S   G   V   F   Q   P   L    99
CTC CTG GAC CTG TCA CAG AAC CAG ATC GCC AGC CTG CCC AGC GGG GTC TTC CAG CCA CTC   456

 A   N   L   S   N   L   D   L   T   A   N   R   L   H   E   I   T   N   E   T   119
GCC AAC CTC AGC AAC CTG GAC CTG ACG GCC AAC AGG CTG CAT GAA ATC ACC AAT GAG ACC   516

 F   R   G   L   R   R   L   E   R   L   Y   L   G   K   N   R   I   R   H   I   139
TTC CGT GGC CTG CGG CGC CTC GAG CGC CTC TAC CTG GGC AAG AAC CGC ATC CGC CAC ATC   576
```

Fig. 22A

```
 Q   P   G   A   F   D   T   L   D   R   L   L   E   L   K   L   Q   D   N   E   159
CAG CCT GGT GCC TTC GAC ACG CTC GAC CGC CTC CTG GAG CTC AAG CTG CAG GAC AAC GAG   636

 L   R   A   L   P   P   L   R   L   P   R   L   L   L   L   D   L   S   H   N   179
CTG CGG GCA CTG CCC CCG CTG CGC CTG CCC CGC CTG CTG CTG CTG GAC CTC AGC CAC AAC   696

 S   L   L   A   L   E   P   G   I   L   D   T   A   N   V   E   A   L   R   L   199
AGC CTC CTG GCC CTG GAG CCC GGC ATC CTG GAC ACT GCC AAC GTG GAG GCG CTG CGG CTG   756

 A   G   L   G   L   Q   Q   L   D   E   G   L   F   S   R   L   R   N   L   H   219
GCT GGT CTG GGG CTG CAG CAG CTG GAC GAG GGG CTC TTC AGC CGC TTG CGC AAC CTC CAC   816

 D   L   D   V   S   D   N   Q   L   E   R   V   P   P   V   I   R   G   L   R   239
GAC CTG GAT GTG TCC GAC AAC CAG CTG GAG CGA GTG CCA CCT GTG ATC CGA GGC CTC CGG   876

 G   L   T   R   L   R   L   A   G   N   T   R   I   A   Q   L   R   P   E   D   259
GGC CTG ACG CGC CTG CGG CTG GCC GGC AAC ACC CGC ATT GCC CAG CTG CGG CCC GAG GAC   936

 L   A   G   L   A   A   L   Q   E   L   D   V   S   N   L   S   L   Q   A   L   279
CTG GCC GGC CTG GCT GCC CTG CAG GAG CTG GAT GTG AGC AAC CTA AGC CTG CAG GCC CTG   996

 P   G   D   L   S   G   L   F   P   R   L   R   L   L   A   A   A   R   N   P   299
CCT GGC GAC CTC TCG GGC CTC TTC CCC CGC CTG CGG CTG CTG GCA GCT GCC CGC AAC CCC  1056

 F   N   C   V   C   P   L   S   W   F   G   P   W   V   R   E   S   H   V   T   319
TTC AAC TGC GTG TGC CCC CTG AGC TGG TTT GGC CCC TGG GTG CGC GAG AGC CAC GTC ACA  1116
```

Fig. 22B

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```
L  A  S  P  E  E  T  R  C  H  F  P  P  K  N  A  G  R  L  L   339
CTG GCC AGC CCT GAG GAG ACG CGC TGC CAC TTC CCG CCC AAG AAC GCT GGC CGG CTG CTC  1176

L  E  L  D  Y  A  D  F  G  C  P  A  T  T  T  T  A  T  V  P   359
CTG GAG CTT GAC TAC GCC GAC TTT GGC TGC CCA GCC ACC ACC ACC ACA GCC ACA GTG CCC  1236

T  T  R  P  V  V  R  E  P  T  A  L  S  S  S  L  A  P  T  W   379
ACC ACG AGG CCC GTG GTG CGG GAG CCC ACA GCC TTG TCT TCT AGC TTG GCT CCT ACC TGG  1296

L  S  P  T  A  P  A  T  E  A  P  S  P  P  S  T  A  P  P  T   399
CTT AGC CCC ACA GCG CCG GCC ACT GAG GCC CCC AGC CCG CCC TCC ACT GCC CCA CCG ACT  1356

V  G  P  V  P  Q  P  Q  D  C  P  P  S  T  C  L  N  G  G  T   419
GTA GGG CCT GTC CCC CAG CCC CAG GAC TGC CCA CCG TCC ACC TGC CTC AAT GGG GGC ACA  1416

C  H  L  G  T  R  H  H  L  A  C  L  C  P  E  G  F  T  G  L   439
TGC CAC CTG GGG ACA CGG CAC CAC CTG GCG TGC TTG TGC CCC GAA GGC TTC ACG GGC CTG  1476

Y  C  E  S  Q  M  G  Q  G  T  R  P  S  P  T  P  V  T  P  R   459
TAC TGT GAG AGC CAG ATG GGG CAG GGG ACA CGG CCC AGC CCT ACA CCA GTC ACG CCG AGG  1536

P  P  R  S  L  T  L  G  I  E  P  V  S  P  T  S  L  R  V  G   479
CCA CCA CGG TCC CTG ACC CTG GGC ATC GAG CCG GTG AGC CCC ACC TCC CTG CGC GTG GGG  1596

L  Q  R  Y  L  Q  G  S  S  V  Q  L  R  S  L  R  L  T  Y  R   499
CTG CAG CGC TAC CTC CAG GGG AGC TCC GTG CAG CTC AGG AGC CTC CGT CTC ACC TAT CGC  1656
```

Fig. 22C

```
 N   L   S   G   P   D   K   R   L   V   T   L   R   L   P   A   S   L   A   E   519
AAC CTA TCG GGC CCT GAT AAG CGG CTG GTG ACG CTG CGA CTG CCT GCC TCG CTC GCT GAG  1716

 Y   T   V   T   Q   L   R   P   N   A   T   Y   S   V   C   V   M   P   L   G   539
TAC ACG GTC ACC CAG CTG CGG CCC AAC GCC ACT TAC TCC GTC TGT GTC ATG CCT TTG GGG  1776

 P   G   R   V   P   E   G   E   E   A   C   G   E   A   H   T   P   P   A   V   559
CCC GGG CGG GTG CCG GAG GGC GAG GAG GCC TGC GGG GAG GCC CAT ACA CCC CCA GCC GTC  1836

 H   S   N   H   A   P   V   T   Q   A   R   E   G   N   L   P   L   L   I   A   579
CAC TCC AAC CAC GCC CCA GTC ACC CAG GCC CGC GAG GGC AAC CTG CCG CTC CTC ATT GCG  1896

 P   A   L   A   A   V   L   L   A   A   L   A   A   V   G   A   A   Y   C   V   599
CCC GCC CTG GCC GCG GTG CTC CTG GCC GCG CTG GCT GCG GTG GGG GCA GCC TAC TGT GTG  1956

 R   R   G   R   A   M   A   A   A   A   Q   D   K   G   Q   V   G   P   G   A   619
CGG CGG GGG CGG GCC ATG GCA GCA GCG GCT CAG GAC AAA GGG CAG GTG GGG CCA GGG GCT  2016

 G   P   L   E   L   E   G   V   K   V   P   L   E   P   G   P   K   A   T   E   639
GGG CCC CTG GAA CTG GAG GGA GTG AAG GTC CCC TTG GAG CCA GGC CCG AAG GCA ACA GAG  2076

 G   G   G   E   A   L   P   S   G   S   E   C   E   V   P   L   M   G   F   P   659
GGC GGT GGA GAG GCC CTG CCC AGC GGG TCT GAG TGT GAG GTG CCA CTC ATG GGC TTC CCA  2136

 G   P   G   L   Q   S   P   L   H   A   K   P   Y   I   *                       674
GGG CCT GGC CTC CAG TCA CCC CTC CAC GCA AAG CCC TAC ATC TAA                       2181
```

Fig. 22D

GCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTA 2260

AGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCG 2339

GTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATGAGGACAGTGT 2418

CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGC 2497

TGGGCTCTCCCACTCCAGGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCG 2576

GCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAAACTGGAAAGGAAGATGCTTTAGGAACATGTTT 2655

TGCTTTTTTAAAATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTGGGAAGATGTTTTTCAAACTCAGAGAC 2734

AAGGACTTTGGTTTTTGTAAGACAAACGATGATATGAAGGCCTTTTGTAAGAAAAAATAAAAGATGAAGTGTGAAAAAA 2813

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 2852

Fig. 22E

```
                1                                                      60
LRSG-1          MCSRVPLLLPLLLLL---ALGP-GVQG------------CPSGCQCS-----QPQTVFC
GPV             M-LRGTLLCAVLGLLR------------------AQPFPCPPACKCVFRDAAQ-----C
IGFBP           MALRKGGLALALLLLSWVALGPRSLEGAEPGTPGEAEGPACPATCACSYDDEVNELSVFC

               61                                                     120
LRSG-1          TARQGTTVPR-DVPPDTVGLYVFENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQ
GPV             SGGDVARISALGLP----------------------TNLTHILLFGMGRGVLQSQSFS
IGFBP           SSRNLTRLPD-GIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGSLEPQALL

              121                                                     180
LRSG-1          PLANLSNLDLTANRLHEITNETFRGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQD
GPV             GMTVLQRLMISDSHISAVAPGTFSDLIKLKTLRLSRNKITHLPGALLDKMVLLEQLFLDH
IGFBP           GLENLCHLHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLEDGLFEGLGNLWDLNLGW

              181                                                     240
LRSG-1          NELRALPPLRLPRLLLLD---LSHNSLLALEPGILDT-ANVEALRLAGLGLQQLDEGLFS
GPV             NALRGIDQNMFQKLVNLQELALNQNQLDFLPASLFTNLENLKLLDLSGNNLTHLPKGLLG
IGFBP           NSLAVLPDAAFRGLGGLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKANVFA

              241                                                     300
LRSG-1          RLRNLHDLDVSDNQLERVPP-VIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVS
GPV             AQAKLERLLLHSNRLVSLDSGLLNSLGALTELQFH-RNHIRSIAPGAFDRLPNLSSLTLS
IGFBP           QLPRLQKLYLDRNLIAAVAPGAFLGLKALRWLDLS-HNRVAGLLEDTFPGLLGLRVLRLS

              301                                                     360
LRSG-1          NLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPP
GPV             RNHLAFLPSALFLHSHNLTLLTLFENPLAEL-PGVLFGEMGGLQELWL-----NRTQL--
IGFBP           HNAIASLRPRTFEDLHFLEELQLGHNRIRQL-AERSFEGLGQLEVLTL-----DHNQLQE
```

Fig. 23A

```
                361                                                                  420
LRSG-1          KNAGRLL--LELDYADFG--CPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTA-PAT
GPV             ----------------------RTLPAAAFRNLSRLRYLGVTLSPRLSA--LPQGAFQGL
IGFBP           VKVGAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLE-GSCLGR--IRPHTFAGL

                421                        *     *      *              * *         *480
LRSG-1          EAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLG---TRHHLACLCPEGFTGLYCES-
GPV             GELQVLALHSNGLTALPDGL-------LRGLGKLRQVSLRRNRLRALPRALFRNLSSLES
IGFBP           SGLRRLFLKDNGLVGIEEQS-------LWGLAELLELDLTSNQLTHLPHQLFQGLGKLEY

                481                                                                  540
LRSG-1          -QMGQGTRPS-PTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNL
GPV             VQLDHNQLETLPGDVFGALPRLTEVLLGHNSWRCDCG-LGPFLG-------WLR-QHLGL
IGFBP           LLLSHNRLAELPADALGPLQRAFWLDVSHNRLEALPGSLLASLG-------RLR--YLNL

                541                                                                  600
LRSG-1          SGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHS
GPV             VGGEEPPRCAG-PGAHAGLPLWALPGGD--AECPGPRGPPPRPAADSSSEAPVHPALAPN
IGFBP           R--NNSLRTFT-PQPPGLERLW-LEGNP--WDCSCPLKALRDFALQNPSAVPR-------

                601                                                                  660
LRSG-1          NHAP------VTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV
GPV             SSEPWVWAQPVTTGKGQDHSPFWGFYFLLLAVQAMITVIIVFAMIK--------------
IGFBP           ------FVQAICEG-DDCQPPVYTYNNITCASPPEVAGLDL------------------

                661                                                                  718
LRSG-1          GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI
GPV             ---IGQLFRKLIRER-ALG-----------------------------------------
IGFBP           --------RDLGEAHFAPC-----------------------------------------
```

Fig. 23B

```
GTCGACCCACGCGTCCGGGAGCCGGAGCCAGAGACCGGGGCTGGGAAACCCCAGCCCGGGACGGGACGCAGCAGCCTCT     79

GGATCCCGGGACCCCGGACCTCTCAGGACCGGCCAGAGGTGAAGGACTGAGGCCCCACTGAGGCCTTGGACCGCACCGC    158

                                                M  H  S  R  S  C  L  P  P  L      10
CTGGCTCCTTCAGCCGCAGTCGTCTCCTGGGACAGAAG ATG CAC TCC AGG AGC TGC CTG CCA CCT CTC     226

 L  L  L  L  L  V  L  L  G  S  G  V  Q  G  C  P  S  G  C  Q                      30
CTG TTG TTG CTT CTG GTG CTC CTG GGG TCT GGA GTA CAG GGT TGC CCA TCA GGC TGC CAG     286

 C  N  Q  P  Q  T  V  F  C  T  A  R  Q  G  T  T  V  P  R  D                      50
TGC AAC CAG CCA CAG ACA GTC TTC TGC ACT GCC CGT CAG GGA ACC ACA GTG CCC CGA GAC     346

 V  P  P  D  T  V  G  L  Y  I  F  E  N  G  I  T  T  L  D  V                      70
GTG CCA CCT GAC ACA GTG GGC CTG TAC ATC TTT GAG AAC GGC ATC ACG ACA CTT GAT GTG     406

 G  C  F  A  G  L  P  G  L  Q  L  L  D  L  S  Q  N  Q  I  T                      90
GGC TGT TTT GCT GGC CTT CCG GGC CTG CAG CTT CTG GAC TTG TCA CAG AAC CAG ATC ACT     466

 S  L  P  G  G  I  F  Q  P  L  V  N  L  S  N  L  D  L  T  A                     110
AGC CTG CCC GGG GGC ATC TTT CAG CCA CTT GTT AAC CTC AGT AAC CTG GAC CTG ACT GCC     526

 N  K  L  H  E  I  S  N  E  T  F  R  G  L  R  R  L  E  R  L                     130
AAC AAA CTG CAC GAG ATC TCC AAC GAG ACC TTC CGT GGC CTG CGG CGC CTG GAG CGC CTC     586

 Y  L  G  K  N  R  I  R  H  I  Q  P  G  A  F  D  A  L  D  R                     150
TAC CTG GGC AAG AAC CGA ATT CGC CAC ATC CAA CCG GGT GCC TTC GAC GCG CTT GAT CGC     646
```

Fig. 24A

```
 L   L   E   L   K   L   P   D   N   E   L   R   V   L   P   P   L   H   L   P   170
CTC CTG GAG CTC AAG CTG CCA GAC AAT GAG CTT CGG GTG TTG CCC CCA TTG CAC TTG CCC   706

 R   L   L   L   L   D   L   S   H   N   S   I   P   A   L   E   A   G   I   L   190
CGC CTG CTG CTG CTT GAC CTC AGC CAC AAC AGC ATC CCA GCC CTG GAA GCC GGA ATA CTG   766

 D   T   A   N   V   E   A   L   R   L   A   G   L   G   L   R   Q   L   D   E   210
GAT ACC GCC AAT GTA GAG GCA TTG AGG TTG GCT GGC CTA GGG CTG CGG CAG CTG GAT GAG   826

 G   L   F   G   R   L   L   N   L   H   D   L   D   V   S   D   N   Q   L   E   230
GGG CTT TTT GGC CGC CTT CTC AAC CTC CAT GAC TTG GAT GTT TCT GAC AAC CAG TTG GAG   886

 H   M   P   S   V   I   Q   G   L   R   G   L   T   R   L   R   L   A   G   N   250
CAT ATG CCA TCT GTG ATT CAA GGC CTG CGT GGC CTG ACA CGC CTG CGG CTG GCT GGC AAC   946

 T   R   I   A   Q   I   R   P   E   D   L   A   G   L   T   A   L   Q   E   L   270
ACC CGT ATT GCC CAG ATA CGG CCC GAG GAC CTC GCT GGT CTG ACT GCC CTA CAG GAA TTG  1006

 D   V   S   N   L   S   L   Q   A   L   P   S   D   L   S   S   L   F   P   R   290
GAT GTG AGC AAC CTA AGC CTG CAG GCC CTG CCC AGT GAC CTC TCG AGT CTC TTT CCC CGC  1066

 L   R   L   L   A   A   A   R   N   P   F   N   C   L   C   P   L   S   W   F   310
CTG CGC CTC TTA GCA GCT GCC AGG AAC CCC TTC AAC TGC TTG TGC CCC TTG AGC TGG TTT  1126

 G   P   W   V   R   E   N   H   V   V   L   A   S   P   E   E   T   R   C   H   330
GGT CCT TGG GTG CGT GAG AAC CAT GTT GTG TTG GCC AGC CCT GAG GAG ACG CGT TGT CAC  1186
```

Fig. 24B

```
 F   P   P   K   N   A   G   R   L   L   L   D   L   D   Y   A   D   F   G   C   350
TTT CCA CCC AAG AAT GCT GGC CGA CTG CTC CTG GAT CTG GAT TAT GCA GAT TTT GGC TGC  1246

 P   V   T   T   T   T   A   T   V   P   T   I   R   S   T   I   R   E   P   T   370
CCA GTC ACC ACT ACC ACG GCC ACA GTA CCT ACT ATA AGG TCT ACT ATC AGG GAA CCC ACA  1306

 L   S   T   S   S   Q   A   P   T   W   P   S   L   T   E   P   T   T   Q   A   390
CTT TCA ACT TCT AGC CAA GCT CCC ACC TGG CCC AGC CTC ACA GAG CCA ACT ACC CAG GCC  1366

 S   T   V   L   S   T   A   P   P   T   M   R   P   A   P   Q   P   Q   D   C   410
TCC ACC GTA CTA TCG ACT GCC CCA CCA ACC ATG AGG CCA GCT CCT CAG CCC CAG GAC TGT  1426

 P   A   S   I   C   L   N   G   G   S   C   R   L   G   A   R   H   H   W   E   430
CCA GCA TCC ATC TGC CTG AAT GGT GGT AGC TGC CGT TTG GGA GCA AGA CAC CAC TGG GAG  1486

 C   L   C   P   E   G   F   I   G   L   Y   C   E   S   P   V   E   Q   G   M   450
TGC CTA TGC CCT GAG GGC TTC ATT GGC CTG TAC TGT GAG AGT CCA GTG GAG CAA GGG ATG  1546

 K   P   S   S   I   P   D   T   P   R   P   P   P   L   L   P   L   S   I   E   470
AAG CCC AGC TCC ATA CCA GAC ACT CCA AGG CCC CCT CCA CTG CTG CCT CTC AGC ATT GAG  1606

 P   V   S   P   T   S   L   R   V   K   L   Q   R   Y   L   Q   G   N   T   V   490
CCG GTG AGC CCC ACC TCC TTG CGT GTG AAG CTG CAG CGC TAC TTG CAG GGT AAC ACT GTG  1666

 Q   L   R   S   L   R   L   T   Y   R   N   L   S   G   P   D   K   R   L   V   510
CAG CTA CGG AGC CTC CGG CTC ACC TAT CGC AAC CTG TCT GGC CCT GAC AAA CGA CTG GTG  1726
```

Fig. 24C

```
 T   L   R   L   P   A   S   L   A   E   Y   T   V   T   Q   L   R   P   N   A   530
ACA TTA CGG CTG CCT GCT TCA CTT GCA GAG TAT ACA GTC ACC CAG CTG CGA CCC AAT GCC  1786

 T   Y   S   I   C   V   T   P   L   G   A   G   R   T   P   E   G   E   E   A   550
ACC TAT TCT ATC TGT GTC ACA CCC TTG GGA GCT GGA CGG ACA CCT GAA GGT GAG GAG GCC  1846

 C   G   E   A   N   T   S   Q   A   V   R   S   N   H   A   P   V   T   Q   A   570
TGT GGG GAG GCC AAC ACT TCC CAG GCA GTC CGC TCT AAC CAT GCC CCA GTT ACC CAG GCC  1906

 R   E   G   N   L   P   L   L   I   A   P   A   L   A   A   V   L   L   A   V   590
CGT GAG GGC AAC CTG CCA CTC CTC ATT GCG CCT GCC CTG GCT GCT GTA CTT CTG GCT GTG  1966

 L   A   A   A   G   A   A   Y   C   V   R   R   A   R   A   T   S   T   A   Q   610
TTA GCC GCT GCA GGG GCA GCC TAC TGT GTG CGG CGG GCA CGG GCA ACT TCT ACA GCT CAG  2026

 D   K   G   Q   V   G   P   G   T   G   P   L   E   L   E   G   V   K   A   P   630
GAC AAA GGG CAG GTG GGG CCA GGG ACT GGA CCC CTG GAA CTA GAG GGG GTG AAA GCC CCT  2086

 L   E   P   G   S   K   A   T   E   G   G   G   E   A   L   S   G   G   P   E   650
TTG GAG CCA GGC TCC AAG GCA ACA GAG GGA GGT GGG GAG GCT TTG TCA GGT GGT CCT GAA  2146

 C   E   V   P   L   M   G   Y   P   G   P   S   L   Q   G   V   L   P   A   K   670
TGT GAG GTG CCT CTT ATG GGC TAC CCA GGG CCC AGC CTT CAG GGG GTC CTC CCT GCT AAG  2206

 H   Y   I   *                                                                   674
CAC TAC ATT TAG                                                                  2218
```

Fig. 24D

ACTGGTGAGAAAGAGCAGCCAGGGGGTCAGGCTTTCAGTCACCACCCTCCTGCTGCCACAGAAGGAAGTTCTCAGTATA 2297

CACCACAGTGCACGTGCATGATGGAGCTGTGGGACCCTCTCTGGGCTGGGTCTCATCTGTAAGCTGCTACAGCCCAGAT 2376

GAACTCTGCCAGCCGCCAGTGCATCCAGTACAGCGCCTGCCATCTTGTGCAATGTGCAACCCTGGGATGTGAGCCCTGC 2455

CATGTGCTGGTAACATGGCTAGGCATGTTGGGCTTCCCAAACCATGGAGTCTGGTAACCAGTGAAGGAAGCCCCCAGAA 2534

ATAATGAGTGGGGAAGGTACTAGGGCACTGGCCTTGGCCTCAAAAGTGCAGGCACACTTGAAACTGGAAAGGAAGGTGC 2613

TCTGGGCACATGTGGATTTGCTTCTATTGTTTTGTTTGTTTTTTCTAATGTATTTATAAAAGATCTTTTCCCATTTAT 2692

GCTGGGAAAGTGTTTTTCAAACTCAGTGACAAGGACTTTGGTTTTTGTAAGACTGTTGATGATATGAAGGCCTTTTGTA 2771

AGAAAATAAAAAATAAAGTAAAAAAAAAAAAAAAAGGGCGGCCGC 2815

Fig. 24E

Replacement Sheet - 09/530,762

```
                10        20        30        40        50
inputs MCSRVPLL-LPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYV
       : ::  :  : :::::. ::.:::::::::::.:::::::::::::::::::::::::.
       MHSRSCLPPLLLLLLVLLGSGVQGCPSGCQCNQPQTVFCTARQGTTVPRDVPPDTVGLYI
                10        20        30        40        50        60

      60        70        80        90       100       110
inputs FENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNET
       :::::: ::.: ::::::::::::::::::.:::.:::::.::::::::::.:::::.:::
       FENGITTLDVGCFAGLPGLQLLDLSQNQITSLPGGIFQPLVNLSNLDLTANKLHEISNET
                70        80        90       100       110       120

     120       130       140       150       160       170
inputs FRGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHN
       :::::::::::::::::::::::::::.:::::::::.:::::.:::::.::::::::::::
       FRGLRRLERLYLGKNRIRHIQPGAFDALDRLLELKLPDNELRVLPPLHLPRLLLLDLSHN
               130       140       150       160       170       180

     180       190       200       210       220       230
inputs SLLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLR
       :. :::.:::::::::::::::::::::::::.:: ::::::::::::::.:.::.:::
       SIPALEAGILDTANVEALRLAGLGLRQLDEGLFGRLLNLHDLDVSDNQLEHMPSVIQGLR
               190       200       210       220       230       240

     240       250       260       270       280       290
inputs GLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNP
       ::::::::::::::.::::::::::::::::::::::.:::.::::::::::::::::
       GLTRLRLAGNTRIAQIRPEDLAGLTALQELDVSNLSLQALPSDLSSLFPRLRLLAAARNP
               250       260       270       280       290       300
```

Fig. 25A

```
     300        310        320        330        340        350
inputs FNCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVP
       :::.:::::::::::::.::.:::::::::::::::::::::::::::.::::::::::
       FNCLCPLSWFGPWVRENHVVLASPEETRCHFPPKNAGRLLLDLDYADFGCPVTTTTATVP
              310        320        330        340        350        360

     360        370        380        390        400        410
inputs TTRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGT
       :.:...:::::  .:: :::: : :.:.:.:..  ::::::. :.:::::::.:.::::.
       TIRSTIREPTLSTSSQAPTWPSLTEPTTQASTVLSTAPPTMRPAPQPQDCPASICLNGGS
              370        380        390        400        410        420

     420        430        440        450        460        470
inputs CHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVG
       :.::.::: .::::::::.::::::.. :: .::..: :::::  : :.:::::::::::
       CRLGARHHWECLCPEGFIGLYCESPVEQGMKPSSIPDTPRPPPLLPLSIEPVSPTSLRVK
              430        440        450        460        470        480

     480        490        500        510        520        530
inputs LQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLG
       ::::::::..:::::::::::::::::::::::::::::::::::::::::.:: :::
       LQRYLQGNTVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSICVTPLG
              490        500        510        520        530        540

     540        550        560        570        580        590
inputs PGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCV
       .::.:::::::::::..::.:::::::::::::::::::::::::::::.:::.::::::
       AGRTPEGEEACGEANTSQAVRSNHAPVTQAREGNLPLLIAPALAAVLLAVLAAAGAAYCV
              550        560        570        580        590        600
```

Fig. 25B

```
     600       610       620       630       640       650
inputs RRGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFP
       ::.:: ...:::::::::::.:::::::::::.:::::::::::..:.:::::::::.:
       RRARA-TSTAQDKGQVGPGTGPLELEGVKAPLEPGSKATEGGGEALSGGPECEVPLMGYP
                 610       620       630       640       650

     660       670
inputs GPGLQSPLHAKPYI
       ::.::. : :: ::
       GPSLQGVLPAKHYI
     660       670
```

Fig. 25C

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```
                1                                                          60
human LRSG-1    MCSR---VPLLLPLLLLLALGP-GVQG-------------CPSGCQCS-----QPQTVFC
murine LRSG-1   MHSRSC-LPPLL-LLLLVLLGS-GVQG-------------CPSGCQCN-----QPQTVFC
GPV             N-LRGTLLCAVLGLLR-------------------AQPFPCPPACKCVFRDAAQ-----C
IGFBP           MALRKGGLALALLLLSWVALGPRSLEGAEPGTPGEAEGPACPATCACSYDDEVNELSVFC

               61                                                         120
human LRSG-1    TARQGTTVPR-DVPPDTVGLYVFENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQ
murine LRSG-1   TARQGTTVPR-DVPPDTVGLYIFENGITTLDVGCFAGLPGLQLLDLSQNQITSLPGGIFQ
GPV             SGGDVARISALGLP-----------------------TNLTHILLLFGMGRGVLQSQSFS
IGFBP           SSRNLTRLPD-GIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGSLEPQALL

              121                                                         180
human LRSG- 1   PLANLSNLDLTANRLHEITNETFRGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQD
murine LRSG-1   PLVNLSNLDLTANKLHEISNETFRGLRRLERLYLGKNRIRHIQPGAFDALDRLLELKLPD
GPV             GMTVLQRLMISDSHISAVAPGTFSDLIKLKTLRLSRNKITHLPGALLDKMVLLEQLFLDH
IGFBP           GLENLCHLHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLEDGLFEGLGNLWDLNLGW

              181                                                         240
human LRSG-1    NELRALPPLRLPRLLLLD---LSHNSLLALEPGILDT-ANVEALRLAGLGLQQLDEGLFS
murine LRSG-1   NELRVLPPLHLPRLLLLD---LSHNSIPALEAGILDT-ANVEALRLAGLGLRQLDEGLFG
GPV             NALRGIDQNMFQKLVNLQELALNQNQLDFLPASLFTNLENLKLLDLSGNNLTHLPKGLLG
IGFBP           NSLAVLPDAAFRGLGGLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKANVFA

              241                                                         300
human LRSG-1    RLRNLHDLDVSDNQLERV-PPVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVS
murine LRSG-1   RLLNLHDLDVSDNQLEHM-PSVIQGLRGLTRLRLAGNTRIAQIRPEDLAGLTALQELDVS
GPV             AQAKLERLLLHSNRLVSLDSGLLNSLGALTELQFH-RNHIRSIAPGAFDRLPNLSSLTLS
IGFBP           QLPRLQKLYLDRNLIAAVAPGAFLGLKALRWLDLS-HNRVAGLLEDTFPGLLGLRVLRLS
```

Fig. 26A

```
                    301                                                 360
human LRSG-1        NLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPP
murine LRSG-1       NLSLQALPSDLSSLFPRLRLLAAARNPFNCLCPLSWFGPWVRENHVVLASPEETRCHFPP
GPV                 RNHLAFLPSALFLHSHNLTLLTLFENPLAEL-PGVLFGEMGGLQELWLNRTQ--------
IGFBP               HNAIASLRPRTFEDLHFLEELQLGHNRIRQL-AERSFEGLGQLEVLTLDHNQ--------

                    361                                                 420
human LRSG-1        KNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAPSP
murine LRSG-1       KNAGRLLLDLDYADFGCPVTTTTATVPTIRSTIREPTLSTSSQAPTWPSLTEPTTQASTV
GPV                 ------L-------------------------RT-------------LPAAAFRNLSR
IGFBP               ------LQEVKVGAF--LGLTNVAVMNLSGNCLRN-------------LPEQVFRGLGK

                    421                 *    *     *          * *        *  480
human LRSG-1        PSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPS
murine LRSG-1       LSTAPPTMRPAPQPQDCPASICLNGGSCRLGARHHWECLCPEGFIGLYCESPVEQGMKPS
GPV                 LRYLGVTLSP-----------------RLSA------LPQGAFQGL-------------
IGFBP               LHSLHLE-GS-----------------CLGR------IRPHTFAGL-------------

                    481                                                 540
human LRSG-1        PTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGS--SVQLRSL-RLTYRNLSGPDKRLV
murine LRSG-1       SIPDTPRPPPLLPLSIEPVSPTSLRVKLQRYLQGN--TVQLRSL-RLTYRNLSGPDKRLV
GPV                 ---GELQVLALHSNGLTALPDGLLR-GLGKLRQVSLRRNRLRALPRALFRNLSSLESVQL
IGFBP               ---SGLRRLFLKDNGLVGIEEQSLW-GLAELLELDLTSNQLTHLPHQLFQGLGKLEYLLL

                    541                                                 600
human LRSG-1        TLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQA
murine LRSG-1       TLRLPASLAEYTVTQLRPNATYSICVTPLGAGRTPEGEEACGEANTSQAVRSNHAPVTQA
GPV                 DHNQLETLPGDVFGALPRLTEVLLGHNSW--------RCDCG-LGPFLGWLRQHLGL---
IGFBP               SHNRLAELPADALGPLQRAFWLDVSHNRL--------EALPGSLLASLGRLR-YLNL---
```

Fig. 26B

```
                601                                                   660
human LRSG-1    REGNLPLLIAPALAAVLLAALAAVGAAY-CVRRGRAMAAAAQDKGQVGPGAGPLELEGVK
murine LRSG-1   REGNLPLLIAPALAAVLLAVLAAAGAAY-CVRRARA-TSTAQDKGQVGPGTGPLELEGVK
GPV             VGGEEPPRCAGPGAHAGLPLWALPGGDAECPGPRGPPPRPAADSSSEAP---------VH
IGFBP           R--NNSLRTFTPQPPGLERLN-LEGNPWDCSCPLKALRDFALQNPSAVP---------R-

                661                                                   720
human LRSG-1    VPLEPGPKATEGGGEALPSGS-ECEVPLMGF-----PGPGLQSP--------------L
murine LRSG-1   APLEPGSKATEGGGEALSGGP-ECEVPLMGY-----PGPSLQGV--------------L
GPV             PALAPNSSEPWVWAQPVTTGKGQDHSPFWGFYFLLLAVQAMITVIIVFAMIKIGQLFRKL
IGFBP           ------------FVQAICEG-DDCQPPVYTYNNITCASPPEVAGLDL----------RDL

                721   728
human LRSG-1    HAKPYI--
murine LRSG-1   PAKHYI--
GPV             IRER-ALG
IGFBP           GEAHFAPC
```

Fig. 26C

```
GAATTCCCGGGTCGACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGGCTGAGCGAAGCGCGGCGGCGGCGGCGG  79

CGCCTAGGGGAGGGAGGGGCGGCGGGGCCGAGCCCACCTAGCGGAGCGCGCCGGCCGCCGGTGGCCGCCGCCAGCATGC  158

CCCGGCCCGCGGGCCGCTCCGCCGCCAGCCACCCCCGCGGCCCTCGGCGGCCTGCGCTCGGCCCGGGGGCGCGGGAACC  237

GCAGCCGGAGCCGGAGGCGGGAGCAGCGAGCCGGAGCCCCGGGCGCTCGAATGCAGGATGCTCGTGGTCCCCAGCATCC  316

TTGAGCCACCAGGAGTGAGGGCTGCTGCTCCCTGAGACCTGGCTCCAAGGAGGATGCCACAGCCGCCTGCCAGCTCCGG  395

          M   S   D   E   R   R   L   P   G   S   A   V   G   W   L   V   C       17
TCTGCACC ATG AGT GAT GAG CGG CGG CTG CCT GGC AGT GCA GTG GGC TGG CTG GTA TGT      454

 G   G   L   S   L   L   A   N   A   W   G   I   L   S   V   G   A   K   Q   K   37
GGG GGC CTC TCC CTG CTG GCC AAT GCC TGG GGC ATC CTC AGC GTT GGC GCC AAG CAG AAG  514

 K   W   K   P   L   E   F   L   L   C   T   L   A   A   T   H   M   L   N   V   57
AAG TGG AAG CCC TTG GAG TTC CTG CTG TGT ACG CTC GCG GCC ACC CAC ATG CTA AAT GTG  574

 A   V   P   I   A   T   Y   S   V   V   Q   L   R   R   Q   R   P   D   F   E   77
GCC GTG CCC ATC GCC ACC TAC TCC GTG GTG CAG CTG CGG CGG CAG CGC CCC GAC TTC GAG  634

 W   N   E   G   L   C   K   V   F   V   S   T   F   Y   T   L   T   L   A   T   97
TGG AAT GAG GGT CTC TGC AAG GTC TTC GTG TCC ACC TTC TAC ACC CTC ACC CTG GCC ACC  694

 C   F   S   V   T   S   L   S   Y   H   R   M   W   M   V   C   W   P   V   N   117
TGT TTC TCT GTC ACC TCC CTC TCC TAC CAC CGC ATG TGG ATG GTC TGC TGG CCT GTC AAC  754

 Y   R   L   S   N   A   K   K   Q   A   V   H   T   V   M   G   I   W   M   V   137
TAC CGG CTG AGC AAT GCC AAG AAG CAG GCG GTG CAC ACA GTC ATG GGT ATC TGG ATG GTG  814

 S   F   I   L   S   A   L   P   A   V   G   W   H   D   T   S   E   R   F   Y   157
TCC TTC ATC CTG TCG GCC CTG CCT GCC GTT GGC TGG CAC GAC ACC AGC GAG CGC TTC TAC  874

 T   H   G   C   R   F   I   V   A   E   I   G   L   G   F   G   V   C   F   L   177
ACC CAT GGC TGC CGC TTC ATC GTG GCT GAG ATC GGC CTG GGC TTT GGC GTC TGC TTC CTG  934

 L   L   V   G   G   S   V   A   M   G   V   I   C   T   A   I   A   L   F   Q   197
CTG CTG GTG GGC GGC AGC GTG GCC ATG GGC GTG ATC TGC ACA GCC ATC GCC CTC TTC CAG  994

 T   L   A   V   Q   V   G   R   Q   A   D   H   R   A   F   T   V   P   T   I   217
ACG CTG GCC GTG CAG GTG GGG CGC CAG GCC GAC CAC CGC GCC TTC ACC GTG CCC ACC ATC  1054

 V   V   E   D   A   Q   G   K   R   R   S   S   I   D   G   S   E   P   A   K   237
GTG GTG GAG GAC GCG CAG GGC AAG CGG CGC TCC TCC ATC GAT GGC TCG GAG CCC GCC AAA  1114

 T   S   L   Q   T   T   G   L   V   T   T   I   V   F   I   Y   D   C   L   M   257
ACC TCT CTG CAG ACC ACG GGC CTC GTG ACC ACC ATA GTC TTC ATC TAC GAC TGC CTC ATG  1174

 G   F   P   V   L   D   S   T   P   I   P   E   R   S   A   V   R   Q   G   E   277
GGC TTC CCT GTG CTG GAC TCT ACG CCC ATC CCC GAA AGG TCT GCA GTG AGA CAG GGA GAG  1234

 D   W   G   K   D   Q   P   E   G   F   H   P   S   S   R   Q   D   C   L   P   297
GAC TGG GGC AAA GAC CAG CCT GAG GGG TTT CAT CCA AGC AGC AGG CAA GAC TGC CTT CCC  1294

 *                                                                               298
TGA                                                                             1297
```

Fig. 27A

GCCATTGCAGGACATGAGGACATGAGCTCCAGAATGGTGCCAGGCCGAGCCCTGTGCCCACAGGTGGTGAGCTTCAGCA 1376

GCCTGCGGGCCGACGCCTCAGCGCCCTGGATGGCACTCTGCGTGCTGTGGTGCTCCGTGGCCCAGGCCCTGCTTCCGAC 1455

CTGTCCTGCCTCAGTTTCCCCATCTGTGATGAGCAGGTGACCACGTTAACTCTCAGGGCTGTTTGAAGTCTCTTGGTTG 1534

TAGGCCCTCGCCACTGAGTGGCCCAGGTGTGAGAGGTAGTCTAGAGCCCTCTGCGGCCTTTGTGGAGGTCCGTTCTCAG 1613

CATGTGGCCTGGTGTGGCTCCCTAGGCCTGAGGCCTCCCACTCTCAGTGCCCCCTGCCCCCTTGGGAACCCACACTCCA 1692

CCCCAGCTAAGCACAACACTGTGGACCACCACCAATGGCACCTGAGCCACCTTGACCACCATTAGTGTCCCCACCCTCA 1771

TTACTCTGCCGTCGTTGCCTGTCCCCACCACATCATCTCCCTCCATGGCTCCCACCATGACGCTGGCAGGTGCAAGCGG 1850

AGAGCACGAGGGCAGCAGGGCCTGGCCTTCCGTGTCCCTGCGTCATCCCCAGCCTCACTCCCCACCCGTGCAGGCCTGG 1929

CCAGGAAGGGATCCTGGCAGGGGCTTCCAGGTTCTCAGCTCAAGGCCTGGTCCCGGGCAGGCGTCCAACCCCTGGGAGC 2008

AATGTATTTCTTTGCCTTCCATCCTGGGCAGACCCCTTACAGGCCTGGGCATTGCCATGGGCCCTGGGTCTTCCCAGGC 2087

TAAGGAGAACCAGGAACAGCTATAACCTTGAGCTAGTGAAATAGGGTAGATGAGAAGGCTGTCTCCTCCAGACCCCTAC 2166

CCCTACACAGTGGCCCCACAATATGAAGACCTGGGGTAATTCCAAGGTGAGCATAGAGCCTGCCTGTGCCCAGTTCCTT 2245

CTGGCCCTCAGGTGGCCAAGCCCATCTCTTCATCCTTCAGATAGGGTCCCACTCCCAGAAGAAGCTGCTGGGGTGGGGG 2324

TGGGAGGCTGCCTAAGCCTGTCTGTGCTTCAGAGGCCCCTCCAGTCCCTGGCTGTGGGGTAACTGGGGGTATGAGCTGT 2403

GGCCACAGGTGAGCAAGGCAGGGAACTGCAATCCAGCCCTGGCCGCGGGAGGGGCCATCTCTGGCCAATGCTGCTGTGC 2482

CTTCAAGGACTGACAAGTTACGTAGGGGCAGAGGTCGCCAGCTAGCCAGTGTCTCCTCCATCTGGGGGGCGTCTGTCCA 2561

CTTGTCACCTTAGGTTTTCACTCATTTGTCACCTTGGGGTTTTGCTCTGTGTGTTTCATATCCAACGGCAATACTTGCA 2640

GGGGGACAGAGTCCTCTAAATACTCCAATCCTGCGGTTTTTACAAACATAAAGGGGGAGACCCCAAGTGGAGGACCCTG 2719

GGCCTGGAGCTCCCTCCCAAACTTTGTCCAGCATCCAGCCTGTTCCCTGGGCTCACTGGGGAGGGAGTTGTCTTCATAG 2798

CACACCCAGAGCCAGGGATCCCTTTGTAGTTTTTTGACAACGGAGCATTTCTCTTCTGTACAGGACCCAATAAAAACTT 2877

CCTTATGATTTGCAAAAAAAAAAAAAAAGGGCGGCCGC 2915

Fig. 27B

```
GAATTCCCGGGTCGACCCACGCGTCCGGCGGCGGGGCCGAGCCCACCTAGCGGAGCGCGCCGGCCGCCGGTGGCCGCCG  79

CCAGCATGCCCCGGCCCGCGGGCCGCTCCGCCGCCAGCCACCCCCGCGGCCCTCGGCGGCCTGCGCTCGGCCCGGGGGC 158

GCGGGAACCGCAGCCGGAGCCGGAGGCGGGAGCAGCGAGCCGGAGCCCCGGGCGCTCGAATGCAGGATGCTCGTGGTCC 237

CCAGCATCCTTGAGCCACCAGGAGTGAGGGCTGCTGCTCCCTGAGACCTGGCTCCAAGGAGGATGCCACAGCCGCCTGC 316

                        M  S  D  E  R  R  L  P  G  S  A  V  G  W  L      15
CAGCTCCGGTCTGCACC ATG AGT GAT GAG CGG CGG CTG CCT GGC AGT GCA GTG GGC TGG CTG      378

 V  C  G  G  L  S  L  L  A  N  A  W  G  I  L  S  V  G  A  K      35
GTA TGT GGG GGC CTC TCC CTG CTG GCC AAT GCC TGG GGC ATC CTC AGC GTT GGC GCC AAG   438

 Q  K  K  W  K  P  L  E  F  L  L  C  T  L  A  A  T  H  M  L      55
CAG AAG AAG TGG AAG CCC TTG GAG TTC CTG CTG TGT ACG CTC GCG GCC ACC CAC ATG CTA   498

 N  V  A  V  P  I  A  T  Y  S  V  V  Q  L  R  R  Q  R  P  D      75
AAT GTG GCC GTG CCC ATC GCC ACC TAC TCC GTG GTG CAG CTG CGG CGG CAG CGC CCC GAC   558

 F  E  W  N  E  G  L  C  K  V  F  V  S  T  F  Y  T  L  T  L      95
TTC GAG TGG AAT GAG GGT CTC TGC AAG GTC TTC GTG TCC ACC TTC TAC ACC CTC ACC CTG   618

 A  T  C  F  S  V  T  S  L  S  Y  H  R  M  W  M  V  C  W  P     115
GCC ACC TGT TTC TCT GTC ACC TCC CTC TCC TAC CAC CGC ATG TGG ATG GTC TGC TGG CCT   678

 V  N  Y  R  L  S  N  A  K  K  Q  A  V  H  T  V  M  G  I  W     135
GTC AAC TAC CGG CTG AGC AAT GCC AAG AAG CAG GCG GTG CAC ACA GTC ATG GGT ATC TGG   738

 M  V  S  F  I  L  S  A  L  P  A  V  G  W  H  D  T  S  E  R     155
ATG GTG TCC TTC ATC CTG TCG GCC CTG CCT GCC GTT GGC TGG CAC GAC ACC AGC GAG CGC   798

 F  Y  T  H  G  C  R  F  I  V  A  E  I  G  L  G  F  G  V  C     175
TTC TAC ACC CAT GGC TGC CGC TTC ATC GTG GCT GAG ATC GGC CTG GGC TTT GGC GTC TGC   858

 F  L  L  L  V  G  G  S  V  A  M  G  V  I  C  T  A  I  A  L     195
TTC CTG CTG CTG GTG GGC GGC AGC GTG GCC ATG GGC GTG ATC TGC ACA GCC ATC GCC CTC   918

 F  Q  T  L  A  V  Q  V  G  R  Q  A  D  H  R  A  F  T  V  P     215
TTC CAG ACG CTG GCC GTG CAG GTG GGG CGC CAG GCC GAC CAC CGC GCC TTC ACC GTG CCC   978

 T  I  V  V  E  D  A  Q  G  K  R  R  S  S  I  D  G  S  E  P     235
ACC ATC GTG GTG GAG GAC GCG CAG GGC AAG CGG CGC TCC TCC ATC GAT GGC TCG GAG CCC  1038

 A  K  T  S  L  Q  T  T  G  L  V  T  T  I  V  F  I  Y  D  C     255
GCC AAA ACC TCT CTG CAG ACC ACG GGC CTC GTG ACC ACC ATA GTC TTC ATC TAC GAC TGC  1098

 L  M  G  F  P  V  L  V  V  S  F  S  S  L  R  A  D  A  S  A     275
CTC ATG GGC TTC CCT GTG CTG GTG GTG AGC TTC AGC AGC CTG CGG GCC GAC GCC TCA GCG  1158

 P  W  M  A  L  C  V  L  W  C  S  V  A  Q  A  L  L  L  P  V     295
CCC TGG ATG GCA CTC TGC GTG CTG TGG TGC TCC GTG GCC CAG GCC CTG CTG CTG CCT GTG  1218

 F  L  W  A  C  D  R  Y  R  A  D  L  K  A  V  R  E  K  C  M     315
TTC CTC TGG GCC TGC GAC CGC TAC CGG GCT GAC CTC AAA GCT GTC CGG GAG AAG TGC ATG  1278

 A  L  M  A  N  D  E  E  S  D  D  E  T  S  L  E  G  G  I  S     335
GCC CTC ATG GCC AAC GAC GAG GAG TCA GAC GAT GAG ACC AGC CTG GAA GGT GGC ATC TCC  1338
```

Fig. 28A

```
 P  D  L  V  L  E  R  S  L  D  Y  G  Y  G  G  D  F  V  A  L   355
CCG GAC CTG GTG TTG GAG CGC TCC CTG GAC TAT GGC TAT GGA GGT GAT TTT GTG GCC CTA  1398

 D  R  M  A  K  Y  E  I  S  A  L  E  G  G  L  P  Q  L  Y  P   375
GAT AGG ATG GCC AAG TAT GAG ATC TCC GCC CTG GAG GGG GGC CTG CCC CAG CTC TAC CCA  1458

 L  R  P  L  Q  E  D  K  M  Q  Y  L  Q  V  P  P  T  R  R  F   395
CTG CGG CCC TTG CAG GAG GAC AAG ATG CAA TAC CTG CAG GTC CCG CCC ACG CGG CGC TTC  1518

 S  H  D  D  A  D  V  W  A  A  V  P  L  P  A  F  L  P  R  W   415
TCC CAC GAC GAT GCG GAC GTG TGG GCC GCC GTC CCG CTG CCC GCC TTC CTG CCG CGC TGG  1578

 G  S  G  E  D  L  A  A  L  A  H  L  V  L  P  A  G  P  E  R   435
GGC TCC GGC GAG GAC CTG GCC GCC CTG GCG CAC CTG GTG CTG CCT GCC GGG CCC GAG CGG  1638

 R  R  A  S  L  L  A  F  A  E  D  A  P  P  S  R  A  R  R  R   455
CGC CGC GCC AGC CTC CTG GCC TTC GCG GAG GAC GCA CCA CCG TCC CGC GCG CGC CGC CGC  1698

 S  A  E  S  L  L  S  L  R  T  S  A  L  D  S  G  P  R  G  A   475
TCG GCC GAG AGC CTG CTG TCG CTG CGG ACC TCG GCC CTG GAT AGC GGC CCG CGG GGA GCC  1758

 R  D  S  P  P  G  S  P  R  R  R  P  G  P  G  P  R  S  A  S   495
CGC GAC TCG CCC CCC GGC AGC CCG CGC CGC CGC CCC GGG CCC GGC CCC CGC TCC GCC TCG  1818

 A  S  L  L  P  D  A  F  A  L  T  A  F  E  C  E  P  Q  A  L   515
GCC TCG CTG CTG CCC GAC GCC TTC GCC CTG ACC GCC TTC GAG TGC GAG CCA CAG GCC CTG  1878

 R  R  P  P  G  P  F  P  A  A  P  A  A  P  D  G  A  D  P  G   535
CGC CGC CCG CCC GGG CCC TTC CCC GCT GCG CCC GCC GCC CCC GAC GGC GCA GAT CCC GGA  1938

 E  A  P  T  P  P  S  S  A  Q  R  S  P  G  P  R  P  S  A  H   555
GAG GCC CCG ACG CCC CCA AGC AGC GCC CAG CGG AGC CCA GGG CCA CGC CCC TCT GCG CAC  1998

 S  H  A  G  S  L  R  P  G  L  S  A  S  W  G  E  P  G  G  L   575
TCG CAC GCC GGC TCT CTG CGC CCC GGC CTG AGC GCG TCG TGG GGC GAG CCC GGG GGG CTG  2058

 R  A  A  G  G  G  G  S  T  S  S  F  L  S  S  P  S  E  S  S   595
CGC GCG GCG GGC GGC GGC GGC AGC ACC AGC AGC TTC CTG AGT TCC CCC TCC GAG TCC TCG  2118

 G  Y  A  T  L  H  S  D  S  L  G  S  A  S  *                  610
GGC TAC GCC ACG CTG CAC TCG GAC TCG CTG GGC TCC GCG TCC TAG                      2163

GACCGCCGGCGCCTCCCCACGGACGCCAGGCAGGCCAGGCCGCTCTCCGGGGCCGCAGCACCAAAGACGCCCGCCTCCC  2242

CCCCGCGCGCAGACATGCGCCACCCCTCCCAGGGGTGAGGGGGCGTTGGCCTCAGCGTTTGTCTTCCGGCTCCTCCCAG  2321

CTGGCCTTGTCCCAGGGGCGACGGCTGCCCCGGACGACTGCGCTGGGCACCGCATGTCCCGGGCCGAGTGAGGTCGGGC  2400

CTGGGGAGCTGAGTGACATCCCAAGCTTGGGCTTGGGTAGTGAGTGACATGTGCACACGTCCAGCTGCGCCATCACCAG  2479

CCCTGCGCAACAGGACGTCGGGAGCAGGGAACCTGAGACAGGGCCACTGCGGGATCGGACAAAGCCCCGCTTTGGAGAG  2558

GCTGAGCTGGAGCCATTGGCCTCCCCAGGGGCTTTCCACCCACACTGCACCATAACCGCCACACCCTTCGGGGGGGGGG  2637

AGGGTACAGAGGGTCTCTAAGCACAGGGGTGTTCAGAGCCCGAACAAGCTTTGATCAGGTTTCCCTGCTTCCGACCTGT  2716

CCTGCCTCAGTTTCCCCATCTGTGATGAGCAGGTGACCACGTTAACTCTCAGGGCTGTTTGAAGTCTCTTGGTTGTAGG  2795
```

Fig. 28B

CCCTCGCCACTGAGTGGCCCAGGTGTGAGAGGTAGTCTAGAGCCCTCTGCGGCCTTTGTGGAGGTCCGTTCTCAGCATG 2874

TGGCCTGGTGTGGCTCCCTAGGCCTGAGGCCTCCCACTCTCAGTGCCCCCTGCCCCCTTGGGAACCCACACTCCACCCC 2953

AGCTAAGCACAACACTGTGGACCACCACCAATGGCACCTGAGCCACCTTGACCACCATTAGTGTCCCCACCCTCATTAC 3032

TCTGCCGTCGTTGCCTGTCCCCACCACATCATCTCCCTCCATGGCTCCCACCATGACGCTGGCAGGTGCAAGCGGAGAG 3111

CACGAGGGCAGCAGGGCCTGGCCTTCCGTGTCCCTGCGTCATCCCCAGCCTCACTCCCCACCCGTGCAGGCCTGGCCAG 3190

GAAGGGATCCTGGCAGGGGCTTCCAGGTTCTCAGCTCAAGGCCTGGTCCCGGGCAGGCGTCCAACCCCTGGGAGCAATG 3269

TATTTCTTTGCCTTCCATCCTGGGCAGACCCCTTACAGGCCTGGGCATTGCCATGGGCCCTGGGTCTTCCCAGGCTAAG 3348

GAGAACCAGGAACAGCTATAACCTTGAGCTAGTGAAATAGGGTAGATGAGAAGGCTGTCTCCTCCAGACCCCTACCCCT 3427

ACACAGTGGCCCCACAATATGAAGACCTGGGGTAATTCCAAGGTGAGCATAGAGCCTGCCTGTGCCCAGTTCCTTCTGG 3506

CCCTCAGGTGGCCAAGCCCATCTCTTCATCCTTCAGATAGGGTCCCACTCCCAGAAGAAGCTGCTGGGGTGGGGGTGGG 3585

AGGCTGCCTAAGCCTGTCTGTGCTTCAGAGGCCCCTCCAGTCCCTGGCTGTGGGGTAACTGGGGGTATGAGCTGTGGCC 3664

ACAGGTGAGCAAGGCAGGGAACTGCAATCCAGCCCTGGCCGCGGGAGGGGCCATCTCTGGCCAATGCTGCTGTGCCTTC 3743

AAGGACTGACAAGTTACGTAGGGGCAGAGGTCGCCAGCTAGCCAGTGTCTCCTCCATCTGGGGGGCGTCTGTCCACTTG 3822

TCACCTTAGGTTTTCACTCATTTGTCACCTTGGGGTTTTGCTCTGTGTGTTTCATATCCAACGGCAATACTTGCAGGGG 3901

GACAGAGTCCTCTAAATACTCCAATCCTGCGGTTTTTACAAACATAAAGGGGGAGACCCCAAGTGGAGGACCCTGGGCC 3980

TGGAGCTCCCTCCCAAACTTTGTCCAGCATCCAGCCTGTTCCCTGGGCTCACTGGGGAGGGAGTTGTCTTCATAGCACA 4059

CCCAGAGCCAGGGATCCCTTTGTAGTTTTTTGACAACGGAGCATTTCTCTTCTGTACAGGACCCAATAAAAACTTCCTT 4138

ATGAAAAAAAAAAAAAAAGGGCGGCCGC 4166

Fig. 28C

```
            1                                                          60
SSTM-1      MS------DERRLPGSAVGWLVCGGLSLLANAWGILSVGAKQKKWKPLEFLLCTLAATHM
SSTM-2      MS------DERRLPGSAVGWLVCGGLSLLANAWGILSVGAKQKKWKPLEFLLCTLAATHM
proteinA-2  MARGGAGAEEASLRSNALSWLACGLLALLANAWIILSISAKQQKHKPLELLLCFLAGTHI
proteinA-3  ------------------------------------------------------------

            61                                                        120
SSTM-1      LNVAVPIATYSVVQLRRQ-RPDFEWNEGLCKVFVSTFYTLTLATCFSVTSLSYHRMWMVC
SSTM-2      LNVAVPIATYSVVQLRRQ-RPDFEWNEGLCKVFVSTFYTLTLATCFSVTSLSYHRMWMVC
proteinA-2  LMAAVPLTTFAVVQLRRQASSDYDWNESICKVFVSTYYTLALATCFTVASLSYHRMWMVR
proteinA-3  ------------------------------------------------------------

            121                                                       180
SSTM-1      WPVNYRLSNAKKQAVHTVMGIWMVSFILSALPAVGWHDTSERFYTHGCRFIVAEIGLGFG
SSTM-2      WPVNYRLSNAKKQAVHTVMGIWMVSFILSALPAVGWHDTSERFYTHGCRFIVAEIGLGFG
proteinA-2  WPVNYRLSNAKKQALHAVMGIWMVSFILSTLPSIGWHNNGERYYARGCQFIVSKIGLGFG
proteinA-3  ------------------------------------------------------------

            181                                                       240
SSTM-1      VCFLLLVGGSVAMGVICTAIALFQTL--------------------AVQVGRQADHRAFT
SSTM-2      VCFLLLVGGSVAMGVICTAIALFQTL--------------------AVQVGRQADHRAFT
proteinA-2  VCFSLLLLGGIVMGLVCVAITFYQTLWARPRRARQARRVGGGGGTKAGGPGALGTRPAFE
proteinA-3  ------------------ITFYQTLWARPRRARQARRVGGGGGTKAGGPGALGTRPAFE

            241                                                       300
SSTM-1      VPTIVVEDAQGKRRSSIDGSEPAKTSLQTTGLVTTIVFIYDCLMGFPVL-----------
SSTM-2      VPTIVVEDAQGKRRSSIDGSEPAKTSLQTTGLVTTIVFIYDCLMGFPVLVVSFSSLRADA
proteinA-2  VPAIVVEDARGKRRSSLDGSESAKTSLQVTNLVSAIVFLYDSLTGVPILVVSFFSLKSDS
proteinA-3  VPAIVVEDARGKRRSSLDGSESAKTSLQVTNLV----------------VSFFSLKSDS

            301                                                       360
SSTM-1      ----------------------------------------------------DSTPI---
SSTM-2      SAPWMALCVLWCSVAQALLLPVFLWACDRYRADLKAVREKCMALMANDEESDDETSLEGG
proteinA-2  APPWMVLAVLWCSMAQTLLLPSFIWSCERYRADVRTVWEQCVAIMSEEDGDDD------G
proteinA-3  APPWMVLAVLWCSMAQTLLLPSFIWSCERYRADVRTVWEQCVAIMSEEDGDDD------G

            361                                                       420
SSTM-1      ------------------------------------------------------------P
SSTM-2      ISPDLVLER--SLDYGYGGDFVALDRMAKYEISALEGGLPQLYPLRPLQEDKMQYLQVPP
proteinA-2  GCDDYAEGRVCKVRFDANGATGPGSRDPA-QVKLLPGR-HMLFP--PL--ERVHYLQVPL
proteinA-3  GCDDYAEGRVCKVRFDANGATGPGSRDPA-QVKLLPGR-HMLFP--PL--ERVHYLQLK-

            421                                                       480
SSTM-1      ERSAVRQGED--------------WGKDQ-------------------------------
SSTM-2      TRRFSHDDADVWAAVPLPA-FLPRWGSGEDLAALAHLVLP-AGPERRRASLLAFAEDAPP
proteinA-2  SRRLSHDETNIFSTPREPGSFLHKWSSSDDIRVLPAQSRALGGPPEYLGQRHRLEDEEDE
proteinA-3  KLDLAAAAAAHTF-----------------------------------FVANPMHLQ-----

            481                                                       540
SSTM-1      ------------------------------------------------PEGFH-----
SSTM-2      SRARRRSAESLLSLRTSALDSGPRGARDSPPGSPRRRPGPGPRSASASLLPDAFALTAFE
proteinA-2  EEA---EGGGLASLRQF-LESGVLGSGGGPP------RGPG-------FFRE--EITTF-
proteinA-3  ------------------------------------------------MRE--DMAKY-
```

Fig. 29A

```
            541                                                        600
SSTM-1      ------------------------------------PSSRQ-----------------
SSTM-2      CEPQALRRPPGPFPAAPAAPDGADPGEAPTPPSSAQRSPGPRP--SAHSHAGSLRPGLSA
proteinA-2 ------------IDETPLPSPTASPGHSPRRPRPLGLSPRRLSLGSPESRAVGLPLGLSA
proteinA-3 ------------------------------------RRMS-----------------

            601                                  642
SSTM-1      ----------------------------------DCL---P
SSTM-2      SWGEPGGLRAAGGGGSTSSFLSSPSESSGYATLHSDSLGSAS
proteinA-2 ------GRRCSLTGGEESARAWGGSWGPGNPIFPQLTL----
proteinA-3 ------GVR--------------------------------
```

Fig. 29B

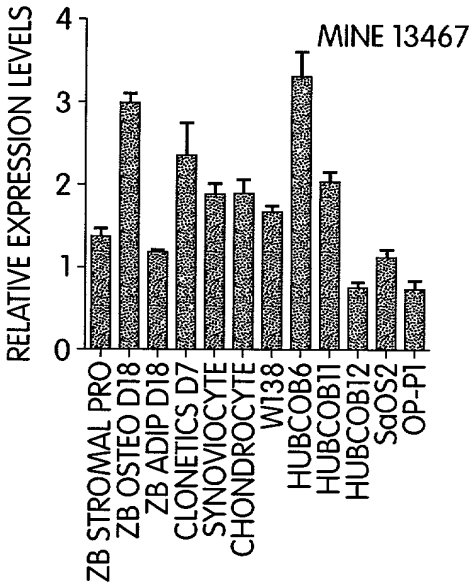

Fig. 30A

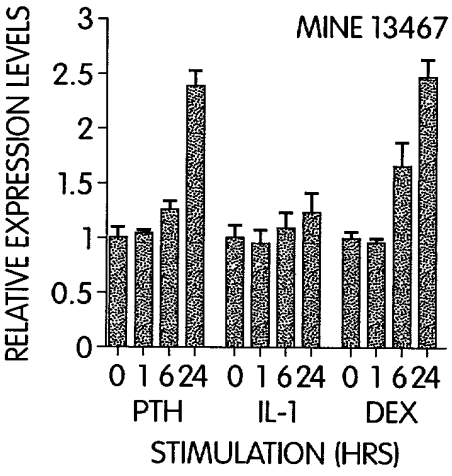

Fig. 30B

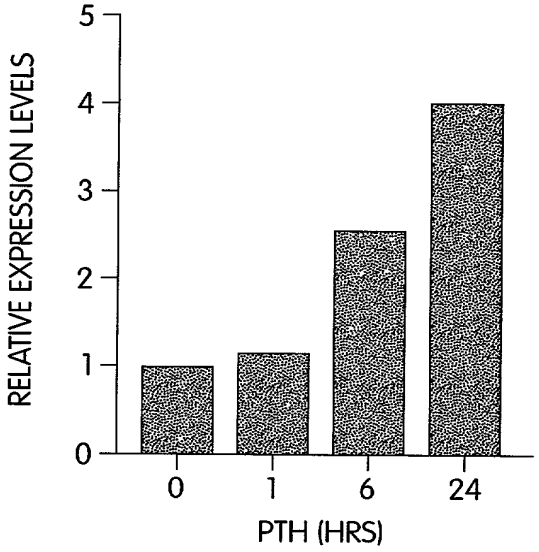

Fig. 30C

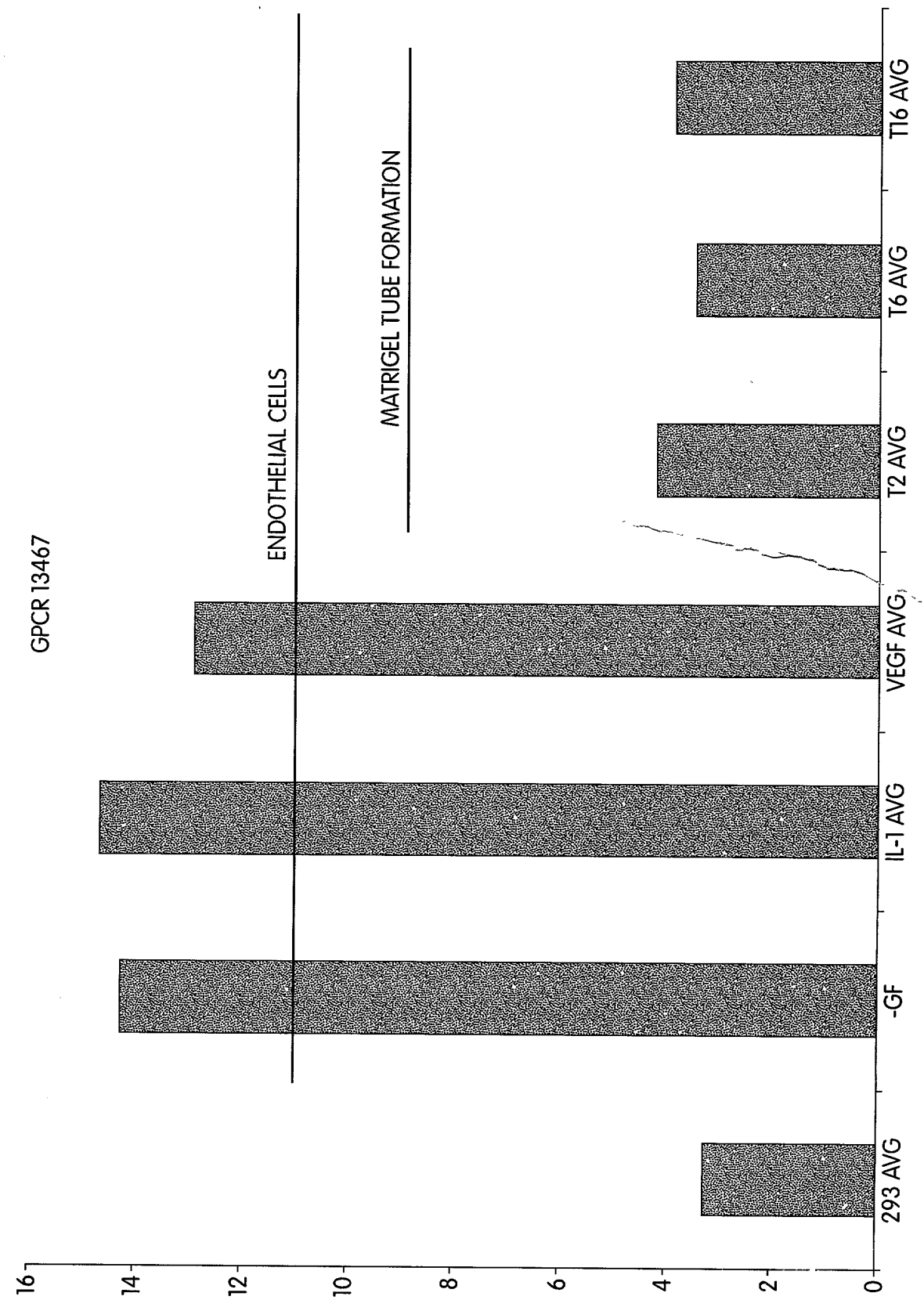
GPCR 13467
ENDOTHELIAL CELLS
MATRIGEL TUBE FORMATION
16
14
12
10
8
6
4
2
0
293 AVG
-GF
IL-1 AVG
VEGF AVG
T2 AVG
T6 AVG
T16 AVG

Fig. 31